```
COCSATOSTO GICAACGANG TOGACOSTOR CCACGROTG ATCAACAAGT TOGCAGGCGA
     COCCOCCTO OCCATOTTOS GAGCOCCGAA COSCCTOGAC COTOCCGAAG ACGCOCGCT
     SUCCECUECC CECECCATAN CCGANCEGOT SECCNACGAG ATGCCCGAGG TCCAAGCCGG
     CATCOMORE GOUGGEOGGE ANATOUTOGE COMCAATUTE GUCGCCAAGE AAAGATYONA
     ATACACAGTO OTOGOCAAGO COOTCAACCA NOCOGOCCGA TTUTGCGAAC TOGCCAAATO
     ACACCCCGCG CGATTGGGTC TOGCCCGCTC GGCTCATGGT CACCCAATTC AAGGACTACT
     TTGGCCTGGC GCACGACCTG CCGAAGTGGG CGAGTGAAGG CGCCAAAGCC GCCGGTGAGG
     COSCEARGE GTTGCCGGCC GCCGTTCCGG CCATTCCGAG TGCTGGCCTG AGCGGCGTTG
     COGCOCCOT COSTCAGGOS SOSTOGOTOS GGGGATTGAA GOTTCOGGCC OTTTGGACCG
10
     DECENCIORADO CTICOSCAAS CTECOSCOST CRTSGOSCOS CEASCOSCOS CONCACACO
     COSCOSCISA ASSITICACA CACGOSTITE GODGATGCO GCICATGGGI ANCGGIGCOG 660
     GACGTGCGTT TAACACTTC GCTGCCCCTC GATACGGATT CAAGCCGACC GTGATCGCCC
     AACCGCCGGC TGGCGGATGA CCARCTACGT TCXTTUATCG AGGATCGAAT TCHACGATTC
     ARAGGRAGA ATTCATATEA CCTCECETTT TATSACEGAT CCECACECNA TNCEGSACAT
15
     COCCOCCCT TTTGAGGTGC ACCCCCAGAC GCTGGAGGAC GAGGCTMGCM GGATGTGGGC
     OFFICE COCA ACATIFICE CIECOGGETO GAGTOGCATO CCCEAGGEGA CUTCONTAGA
     CACCATEGOC CAGATGAATC AGGCGTTTCN CAACATGGTG AACATGCTGC ACGGGGTGNG 1020
     TEACGGGCTG OTTCGCCACG CCAACAACTA CGAACAGCAA GAGCAGGCCT CCCAGCAGAT 1080
     CTTCAGCAGC TGACCCGGCC CGACGACTCA GGAGGACACA TGACCATCAA CTATCAATTC 1140
20
     GGGGACGTCG ACCCTCATGC CGCCATGATC CGCGCTNTGG CCGGGTTGCT GGAGGCCGAS 1200
     CAPCAGECCA TOATTTOTGA TGTGTTGACC GCGAGTGACT TTTGEGGCGG CGCCGGTTCG 1260
     SCORCUTGCC ASSOCTICAT TAUCCASTIG GGCCDTAACT TCCAGGIGAT TTACGAGCAG 1320
     GCCAACGCC ACEGGCAGAA GGTGCAGGCT GCCGGCAACA ACATGGCACA AACCGACAGC 1380
     SCOSTNESST CONSCIONACCONSCIONACTIC SCICCOCCO GOSCOGGCCS 1440
     ATCACCOTOS ACTITOSCOS COSATACACO GOCATATENE NOTOSGGAAC ACTGOSCOCO 1800
     COTCASNICC COCCTICCC TICTINGSCS ACCISCICS IGAISSCIII GACGACCOCI 1560
     TOGOCGGOGO GGCCAATCAA TIGGIOGOGO TIGCOINTAG COCATIOGIG CGACGCCCCC 1630
     GBODCCECGA GTTGTCCCTT GAAATAASGA ATCACAGCAC GGGCGAACAG CTCATAGGAG 1890
     TGAAAGGTTG CCUTGGCGGG GCCC
                                                                                      1704
30
     (2) INFORMATION FOR SEC ID NO:9:
           (i) SEQUENCE CHARACTERISTICS:
                 (A) LEMOTH: 2286 base pairs
35
                 (B) TYPE: nucleic soid
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear
          (ii) MOLECULE TYPE: DNA (genomic)
40
          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:
     COSTCTTSGC STCTSGGCGC ATTSTSATCT SGGCCANTTG CCCCTCCACC CAGACCGCGC
                                                                                       50
     CCAGCTTOTC GATCCAGCCC GOGACOCGGA TTGCCACCGC GOGAACCGGG AACGGATTCT
                                                                                      120
     CCGCTGAATT CTGGGTCACT TCGCAGTCGC GCGGGTGATC CTGTTGGCGA NCAGCGTCTG
                                                                                       0.80
                                                                                      240
     GAACGGGCUT CHAACGCGTG CCGTAAGCCC AGCGTGTACG CCGTCAGCCC GACGCCGATG
                                                                                      390
     CCGAATGCCT TGCCGCCCAA GCTGAGCCGC GCGGGCTCCA CCAAGAGCGT CACGGTGAGC
     CAGCCAACCA GATGCAAGGC GACGATCACC GCGAAGTGCC GAATTCGGCA CGAGAGGTGC
TGGAAATCCA GCAATACGCC CGCGAGCCGA TCTOGTTGGA CCAGACCATC GGCGACGANG
                                                                                      360
                                                                                      420
     GCGACAGNCA GCTTGGCGAT TTCATCGAAA ACAGCGAGGC GGTGGTGGNC GTCGACGCGG
                                                                                      480
     TOTACOTTCAC TITTOCTOCTAT TICATCOARA ACAGCGAGGC GSTSSTSGNC GTCGACGCGG
TGTCCTTCAC TITTOCTOCAT GATCAACTGC ANTONOTOCT GGACACGCTC TCCGAGGGTG
AGGCGGGCGT GGTGCGGCTA CGCTTCGGCC TTACCGACCG CCAGCCGCGC ACCCTTGACG
AGATCGGCCA GGTCTACGGC GTGACCCGGG AACGCATCCG CCAGATCGAA TCCAAGACTA
TGTCGAAGTT GCCCCATCCG AGCCGCTCAC AGGTCCTGCG CGACTATCGT GCCGAATTCG
GCACGAGCCG TTTTGAGGTG CACGCCCAGA CGGTGGAGGA CGAGGCTCGC CGGATGTGGG
CGTCCGCGCA AAACATTTCC GGTGCGGGCT GGAGTGGCAT GGCCGANGCG ACCTCGCTAG
ACACCATGGC CCAGATGAAT CAGGCGTTTC GCAACATCGT GAACATGCTG CACGGGGTGC
GTGACGGGCT GGTTCGCGAC GCCAACAACT ACGAACAGCA AGAGCAGGCC TCCCAGCAGA
                                                                                      340
                                                                                      600
                                                                                       660
                                                                                       720
                                                                                      780
840
```

900 960

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TCCTCAGCAG CTGACCCGGC CCGACGACTC AGSAGGACAC ATGACCATCA ACTATCAATT 1920
    CRESCACOTC GACOCTCATO OCCICCATGAT CCGCOCTCTG OCCOGOTTGC TGGAGGCCGA 1080
    OCATCASSCC ATCATTTCTS ATSTSTTSAC CSCSAGTGAC TTTTGSSSCS GCGCCGGTTC 1140
    GGCGGCCTGC CASGGGTTCA TTACCCAGTT GGGCCGTAAC TTCCAGGTGA TCTACGAGCA 1200
    GGCCAACGCC CROGGCAGA AGUTGCAGGC TGCCGGCAAC AACATGGCAC AAACGGACAG 1260
    COCCOTCGGC TCCAGCTGGG CCTAACCCGG GTCCTAAGTT GGGTCCGCGC AGGGCGGGGC 1326
    GATCAGCETC GACTITGGCG CCCGATACAC GGGCATEING INSICGGGAA CACTGCGCCC 1386
    OCCICAGOTO OCCOCTICOO CITOTICOGO CACCITOCICO CIGATOCCIT TOACCACCOC 1440
    TICOCCOGCO COGCCAATCA ATTOGICOCO CITOCCICTA GCCTCOTGCC GAATTCOGCA 1800
10
    CGASSOTSCT GOTGCCSCGC TATCSSCAGC ACGTGASCTC CACGACGAAC TCATCCCAGT 1550
    GCTGGGTTCC GCGGASTTCG GCATCGGCGT GTCGGCCGGA AGGGCCATCG CCGGCCACAT 1620
    COCCOCTCAA GCCCGCTTCG ASTACACCST CATCGGCGAC CCCGTCAACG AGGCCGCCCG 1680
    OCTCACCOAA CTOSCCAAAG TCOACOATOS CCACGTTCTG GCOTCGGCGA TCGCGGTCAG 1740
    TGGCGCCCTG GACGCCGAAG CATTGTGTTG GGATGTTGGC GAGGTGGTTG AGCTCCGCGG 1800
35
    ACCITECTECA COUNCOURAC TAGOCAGGOO BATGAATNIG CONGCACOOG BAGAGGITIIC 1850
    CASCGAAGTA CSCSSCTAGT CSCSCTTSSC TGCSTTCTTC GCCSGCACCT TCCGGGCASC 1920
    TTTCCTGGCT GGCGGTTTTG CGGGACCCCG GGCTGGGCGA TCGGCCAACA GCTGGGCGGC 1980
    GOSCTOSTOS STIATOGAAS CCACSTESTO SCCCTTACOC ASSCTSSCAT TSSTCTCACC 2040
    GTCSGTGACS TACGGCCCGA ATCGGCCSTC CTTGATGACC ATTGGCTTGC CAGACGCCSS 2100
    ATNIGHTOCC AGCIOGOGCA GCGGGGGAGC CGAAGCGCII TGCCGGCCAC GACNITICGG 2160
    CTCTGMGTAG ATMTTCAGGG CTTCGTCGAG CGMGATGGTG AATATATGGT CTTCGGTGAC 2220
    CASTGATONA GAATOTTIGO COCCOTTIAS ATACGGTONG TAGOGCOCT TOTGCGCGGT 2280
                                                                      2286
23
   (3) INFORMATION FOR SEQ ID NO:10:
         (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1136 base pairs
              (B) TYPE: nucleic soid
30
```

- (C) STRANDSDNESS: single
- (D) TOPOLOGY: linear
- (ii) NOLECULE TYPE: DNA (genomic)
- 35 (xi) SEQUENCE DESCRIPTION: SEQ ID No:10:

	CCCCATCTTC	CCCGACCGCG	CCTCGATCAT	CCGCCTCGTC	GGAGCCGTCC	TOGCOGRACA	60
	ACACGACGAA	TOGATOGAAG	GACGGCGCTA	CCTGGGCCTC	GAGGTCCTCA	CCCGAGCCCG	130
	AGCAGCACTO	ACCAGCACCO	AAGAACOGCC	AAGCAGCAAA	CCACCRACAC	CCCAGÇACTG	383
40	ACCACCTAGA	CTGCCACCCG	AAGGATCACG	CGAGGAACCT	TCACTCGTAC	ACCACGTCCC	240
	TOGCCTTGGC	CTGGTGTCAG	GCCCAGCTGG	AGCCGACGGC	GCTGTCGGTT	TGCGCCATGT	300
	TGTTGCCGGC	AGCCTGCACC	TTCTGCCOST	GGGCGTTGGC	CTGCTCGTAG	ATCACCTOGA	360
	AGTTACGGCC	CAACTOGGTA	ATGAACCCCT	GGCAGGCCGC	CGRACCGGCG	COSCOCCAAA	420
	AGTCACTCGC	GOTCAACACA	TCACGAATGA	TGGCCTGATG	CTCGGCCTCC	AGCAACCCGG	480
45	CCTGAGCGCG	GATCATGGCG	CCGTGAGCCT	CUACATCACC	GAACTGATAG	TTOATGGTCA	840
	TOGRACCIOT	TCTCCTTCGC	TTGTAAAAGT	ATTGTGCTGC	AGCGGCTGAC	GTTAGCTGCT	600
	GAGGATCTGC	TOGGAGGCCT	GCTCTTGCCT	CGTGCCGAAT	TOGGCACGAG	AGGCCGCCTT	660
	CGAAGAAATC	CTTTGAGAAT	TCGCCAAGGC	COTTCGACCCA	GCATGGGGTC	AGCTCGCCAG	720
	CCGCGCCCGGC	TGGCAACCGT	TCCCGCTCGA	GAAAGACCTG	GAGGAATACC	AGTGACAAAC	780
50	GACCICCCAG	ACGTCCGAGA	GCGTGACGGC	GGTCCACGTC	CCGCTCCTCC	TOCTOGCGGG	\$40
	CCACGCTTGT	CAGACGTGTG	GGTTTACAAC	GGGGGGGGGT	ACGACCTGAG	TGAGTGGATT	900
	TCCARGCATC	ccaacaacac	CTINTICATI	GOGCGGACCA	AGAACCGGA	CATCACCGCA	960
	ATCGTCAAGT	CCTACCATOS	TOATCCGGCG	ATTOTCOAGC	GRATCCTGCA	GCGGAGGTAC	1020
	GCGTTGGGCC	GCGACGCAAC	CCCTAGGGAC	ATCCACCCCA	ACCACAATGC	ACCEGERATE	1080
55	CTGTTCAAAG	ACCRCTTCAR	CAGCTOGCGG	GACACCCCCGA	AGTATOGATY	MOACOA	1136

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

```
(A) LENGTH: 967 base pairs
                (B) TYPE: nucleic soid
                (C) STRANDEDNESS: single
 5
                (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: DEA (genomic)
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:
10
                                                                              60
     TGAGCGCCAA CCCTACCSTC GGTTCGTCAC ACGGACCGCA TGGCCTGCTC CGCGGACTGC
                                                                             320
     CECTAGGGTC GCCGATCACT CGGCGTAGCG GCGCCTTTGC CCACCGATAT GGGTTCCGTC
     ACAGTGT9DT TGCCCGCCCG CCATCGGCCG GATAACGCCA TGACCTCAGC TCGGCAGAAA
                                                                             2,80
     TEACAATECT CCCAAAGECE TEAGCACCCE AAGACAACTA AGCAGGAGAT CECATGCCFT
                                                                             240
     TTOTGACTAC CCAACCAGAA GCACTGGCSG CGGCGGCCGG CASTCTGCAG GGAATCGGCT
                                                                             300
     COSCATTSAA CSCCCAGAAT SCSSCTGCSS CSACTCCCAC GACGSSGSTS STCCSSCSSC
                                                                             360
     COCCUATGAA MIGTCOSCOC TGACOGODSC TCAGTTOSCS GCACACGCCC AGATCTATCA
     GGCCGTCAGC GCCCAGGCCG CGGCGATTCA CGAGATGTTC GTCAACACTC TACAGATGAG
                                                                            480
     CTCASGOTOG TATECTECTA CCGAGGCCEC CAACGCGGCC GCGGCCGGET AGAGGAGTCA
   CTGCGATGGA TTTTGGGGGG TTGCCGCCGG AGUTCAATTC GGTGCGGATG TATGCCGTTC
     CTGGCTTGGC ACCAATGCTC GCTGCGGCST CGGCCTGGAA CGGGTFGGCC GCGGAGCTGA
     CTTCGGCGGC CACCGGTTAT GAGACGGTGA TCACTCAGCT CASCAGTGAG GGGTGGCTAG
     STOCEGOSTO ACCOCCENTO SCOGREGORO TECCECOSTA TETEGOCOTES ATGRETECOS
     CTSCGGCGCA AGCCGAGCAG GCCGCCACAC AGGCCAGGCC CGCCGGGCC GCTTTTGAGG
     CGGCGTTTGC CGCGACGGTG CCTCCGCCGT TGATCGGGGC CAACCGGGCT TCGTTGATGC
     AGCTGATCTC GACGAATGTC TTTGGTCAGA ACACCTCGGC GATCGCGGC GCCGAAGCTC
                                                                             960
     ACTACCC
                                                                              967
     (2) INFORMATION FOR SEQ ID NO:12:
30
          (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 585 base pairs
                (B) TYPE: nucleic acid
                (C) STRANDEDNESS: single
35
                (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: DNA (genomic)
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:
40
     TGGATTCCGA TAGCGGTTTC GGCCCCTCGA CGGGGGACCA CGGGGGGGAG GCCTCCGAAC
                                                                              80
     GOGGGGCCGG GACGCTGGGA TTCGCCGGGA CCGCAACCAA AGAACGCCGG GTCCGGGCGG
                                                                              1.20
     TOGGGCTGAC COCACTGGCC SGTGATGAGT TCEGCAACGG CCCCCGGATG CCGATGGTGC
                                                                              180
     COCOCACCTO COACCACCOC ACCAACGASC CCCACCCCC CGACCGATCC COCAGAGGGGG
                                                                              240
     GAGGCGACGG CTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCACGT GGACCCGTAC
GGGTCGAAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCCACAG TTGGTGGCCT
CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCGGCA CACGATCGGT CAGGCCGAGC
                                                                             300
                                                                             380
                                                                             420
     AGGCSSCOAT GYCGGCYCAG GCDYYYCACC AGGGGGAGYC GYCGGCGGGG TYYCAGGCCG
                                                                             480
     COCATGCCCG OTTTOTOGGG GCGGCCGCCA AAOTCAACAC CITGTTGGAT OTCGGGCAGG
                                                                             840
50
     CGAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTG
                                                                              $85
     (2) INFORMATION FOR SEC ID NO:13:
          (1) SEQUENCE CHARACTERISTICS:
35
               (A) LENGTH: 144 amino acids
                (B) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
```

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13: 5 Ala Leu Val Thr Thr Asn Phe Phe Gly Val Asn Thr Ile Pro Ile Als 10 Lew Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gln Ala Ala Thr Val 2.5 10 Met Ser His Tyr Gin Ala Val Ala His Giu Ile Trp Cys Leu His Glu 8.0 Xaa Ala Ser Ser Gly Lys Pro Trp Ala Ser Ile Thr Thr Gly Ala Pro 88 Gly Ser Pro Alm Ser Thr Thr Arg Ser Arg Thr Pro Leu Val Ser Thr 15 70 7.5Asn Arg Xaa Val Xsa Ala Pro Ile Val Ser Pro Asn His Thr Cly His 20 Arg Pro Clu Lys Cly Lou Cly Ser Xaa Cln Arg Arg Lou Ser Arg Val 105 20 Leu Pro Arg Ile Ile Asp Arg Pro Ala Gly Pro Xaa Gly Pro Pro Lou 120 Thr Sar Gly Ser His Phe Leu Cys Ser Trp His Gly Tyr Ser Ser Gla 25 (2) INFORMATION FOR SEQ ID NO:14: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 352 amino acids (B) TYPE: smino acid 30 (C) STRANDEDWESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 35 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16: His Ala Leu Ala Ala Gln Tyr Thr Glu Ile Ala Thr Glu Leu Ala Ser Val Leu Ala Ala Val Glo Ala Ser Ser Trp Glo Gly Pro Ser Ala Asp 40 28 Arg Phe Vel Val Ala His Gln Bro Phe Arg Tyr Trp Leu Thr His Ala Ala Thr Val Ala Thr Ala Ala Ala Ala Ala His Xee Thr Ala Ala Ale 45 Gly Tyr Thr Ser Ala Leu Cly Cly Met Pro Thr Leu Ala Clu Leu Ala Ala Asn His Ala Met His Gly Ala Leu Vol Thr Thr Asn Fhe Fhe Gly Val Aso Thr Ile Pro Ile Ala Leu Aso Glu Ala Asp Tyr Leu Arg Met 50 1.08 Trp Ile Gln Ala Ala Thr Val Het Ser His Tyr Gln Ala Val Ala His 120 Giu Ser Val Ala Ala Thr Pro Ser Thr Pro Pro Ala Pro Gln Ile Val 135 55 Thr Ser Ala Ala Ser Ser Ala Ala Ser Ser Ser Pho Pro Asp Pro Thr 155 Lys Leu Ile Leu Gln Leu Leu Lys Asp Phe Leu Glu Leu Leu Arg Tyr

	Leu	Ala	Val	Glu 180	Leu	Leu	Pro	Gly	Pro 185	Leu	oly	Asp	Leu	Tle 190	Ala	Gln
	Val	Leu	Asp 195	Tro	Phe	Ile	Ser	Phe 200	Val	Ser	Gly	Pro	Val 208	Phe	The	Phe
5	Leu	Ala 210	Tyr	Leu	Val	Leu	Asp 235	bro	Leu	Ile	Tyr	Phe 220	Gly	\$ro	Phe	Ala
	Pro 228	1466.83	Thr	Ser	Pro	V&1 230	Leu	Leu	Pro	Ala	Val 235	Glu	Leu	Arg	Asn.	Arg 240
10	Leu	Lys	Thr	Ala	Thr 245	Gly	Leu	Thr	Leu	Pro 250	Pro	Thr	Val	lle	Phe 255	Asp
	His	Pro	Thr	Pro 260	Thr	Ala	Val	Ala	01u 265	Tyr	Val	Ala	Gla	91n 270	Met	Sex
	gly	Ser	Arg 275	Pro	Thr	Ģlu	Ser	Gly 280	Asp	Pro	Thr	Ser	Gln 285	Val	Val	Glu
15	Pro	Ala 290	Arg	Ala	Glu	Pho	Gly 295	Thr	Ser	Ala	Val	His 300	Gln	Ile	Pro	Pro
	Axg 305	Pro	Ala	Asp	Thr	Arg 310	Arg	Ala	Cys	Arg	His 315	Arg	Asp	Asp	Val	920 320
20	Arg	Asp	Ser	Arg	Ile 325	Ala	Gin	His	Arg	Asp 330	Gly	Ala	01y	beu	Asp 335	pro
	Thx	Glu	Arg	Gly 340	The	Ser	Glu	Gly	Asp 345	Gln	Gly	Leu	Val	Ser 350	Gly	Trp

	(2)	infoi	CZAMS	ON I	FOR S	(Ç31	D N):18:	š								
i,		(1)	(A) (B) (C)	LEI TYI STI	i chi icth: 7E: 2 Iandi 701.C	: 14) emino enses	lam Saci	ino a id sing:	acida	3							
10		(11)	NOW	scvili	TY!	PS: j	ept.	ide									
		(xi)	SRQ	IENCI	e des	CRII	PTIO)	\$; \$)	8Q II) NO:	:15:						
		Met 1	qaA.	Phe	Gly	Ala S	Leu	Pro	Pmo	Glu	Val 10	Asn	Ser	Val	Arg	Met 19	Tyn
15		Ala	Val	Pro	Gly 20	Sex	Ala	bro	Met	Val 25	Ala	Ala	Ala	Sar	Ala 30	Trp	Ası
		Øly	læu	Ala 35	Ala	Glu	Leu	Sex	Ser 40	Als	Ala	rair	Gly	Tyr 45	Glu	Thr	Val
20		Tle	Thr S0		Leu	Ser	Ser	Glu SS		Trp	Leu	Gly	Pro 60	Ala	Ser	Ala	Als
		Met 68		Glu	Ala	Val	Ala 70		Tyx	Val	Als	Trp 75		Ser	ala	Ala	Ala 80
			Gln	Ala	Glu	Gla 85		Älä	Thr	Gln	Ala 90		Als	Ala	Ala	Ala 95	
25		Phe	Glu	Ala	Ala 100		Ala	Als	Thr	Val 105		Pro	Pro	Leu	11e	Ala	ale
		Asn	Ang	Ala 115		Leu	Met	Gln	Leu 120		Ser	Thr	Asn	Val 128		Gly	Gli
30		Asn	Thr 130		Ala	Ils	Ala	Ala 135		Glu	Ala	Gln	Tyr 140			•	
	(2)	INFO	rmatt:		TOR I	e oraș		0:16:	ı								
35		(i)	SEQ! (A) (B) (C)	JENC) LEI TYI	: CH2 NGTH: PE: : NAMDI POLO:	RAC : 58 :min: :DNE:	reri: emi: dac: se: :	STIC: SO A: id sing:	3: Mids								
\$ ()		(11)	MOL	cor	TYI	?83: {	ept:	ide									
		(xi)	SEQ	meci	e de	Kari	TIO	18 : 1833	e ii) 180:	:16:						
45		Met 1	Ala	Ser	Arg	Phe 5	Met	Thr	Asp	Pro	Nis 10	Ala	Met	Arg	qsA	Met 15	ilā
		Gly	Arg	Phe	30 31:0	Val	His	Ala	Gln	Thr 25	Val	Glu	Asp	Glu	Ala 30	Arg	Ary
		Met	Trp	Ala 35	Sex	Als	Gin	Asn	Ile 40	Ser	ĠĬŸ	ala	Gly	Trp 45	Ser	Gly	Met
50		Ala	Slu S0	Ala	Thr	Ser	Leu	Asp 55	Thr	Met	Thr						
	(2)	INFO	emat:	ION I	FOR S	er Cer	ed n	0:17:	:								
55		(i)	(A) (B)	LE!	e chi igth: pe: : tandi	: 67 amino	ami Se c	oo aa id	sids								

			$\langle \mathfrak{Q} \rangle$	TO	90T08	3Y: :	linea	3.1°									
5		(ii) (xi)							eg II	or c	:17:						
w.f		Met. 1	Thr	Tle	Asn	Tyr S	Gla	Pho	sly	Asp	Val 10	Asp	Ala	His	aly	Ala 15	Med
			Arg	Ala	31n 20	Als	Ala	Ser	Leu	Glu 25		Glu	His	Gln	Ala 30		Val
10		Arg	Asp	Val 35	žeu	Ala	Xla	Gly	Asp 40	Phe	Trp	gly	Sly	Ala 45	Gly	Ser	Va)
			50	Gla	Olu	Pha	Il»	Thr 55	Gln	Leu	Gly	Arg	Asn 60	Phe	Gln	Val	Lle
15		Tyx 65	glu	Gln													
	(2)	INFO	RMAT:	ION :	POR :	SEQ :	n n	0:38	\$								
20		\$\$.}	(A) (B) (C)	Jenci Lei Tyi Sti	KANDI	: 58 amin: EONE:	ami: o ac: ss:;	so a: id sing:	cids								
25		(11)	350E	scun	e TY	PS: 1	pept:	ide									
		(x1)	SEQ)ENC:	e de:	ecri:	PTIC	s: Si	eQ II	o no	:18:						
30		Met 1	Ala	Ser	Arg	Phe S	Met	Max	Asp	Pro	Bis 10	Als	Met	Arg	Asp	Met 15	Ale
		Gly	Arg	Phe	Glu 20	Val	Ris	Ala	Gln	Thr 25	Val	Glu	Asp	Ølu	Ala 30	Arg	Arg
				Ala 35					40			Alm	Gly	Trp 45	Ser	Gly	Met
35		Ala	6), u 50	Ala	Thr	ger.	Leu	Asp 55	Thr	Met	The						
	(2)	INFO	rmat'	eom i	for i	98Q (e e	7:19	3								
40 45		(i)	(A) (B) (C)	JENCI LSI TYI STI TOI	goth 20: : 20: :	: 94 smin: BONE:	ami) ac: 98: :	no a: id sing:	ciás								
₩ _};		(ii)	MODA	sculi	ryi	PE: j	pept.	ide									
		(kx)	SEÇ	JENCI	e de	BCRI	PTIO	I: SI	Q II	OM C	: 19:						
50		Met	Thr	Ile	Asn	Tyr 5	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala 15	Met
			Arg	Als	Gln 20		Ala	Sex	Leu	Glu 25		Glu	Nis	Gln	Ala 30		Val
55		Arg	Asp	Val 35	Lett	Ala	Ala	Gly	Asp 40	Phe	Trp	Gly	Gly	Ala 45	Gly	Ser	Va.)

Ala Cys Gln Glu Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile

Tyr Glo Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn

80

70

68

Asn Met Ala Gin Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 8.5 (2) INFORMATION FOR SEQ ID NO:20: (1) SEQUENCE CHARACTERISTICS: (A) LEWGTH: 30 amino acids (B) TYPE: amino acid 10 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20: Asn Met Leu Ris Gly Val Arg Asp Gly Leu Val Arg Asp Ala Asn Asn 10 Tyr Glu Gin Gin Glu Gin Ala Ser Gin Gin Ile Leu Ser Ser 20 (2) INFORMATION FOR SEQ ID NO:21: (i) SEQUENCE CHARACTERISTICS: 25 (A) LENGTH: 94 amino acids (B) TYPE: amino acid. (C) STRANDEDNESS: single (D) TOPOLOGY: linear 30 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21: Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 35 30 Ile Ary Ala Gln Ala Gly heu beu Glu Ala Glu His Gln Ala Ile Ile 38 Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala & Ø 40 Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile \$ 8 Tyr Glu Gln Ala Aso Ala Kis Gly Gln Lys Val Gln Ala Ala Gly Aso 70 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 45 90 (2) INFORMATION FOR SEQ ID NO:22: (i) SEQUENCE CHARACTERISTICS: 50 (A) LENGTH: 59 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 33 (ii) NOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 22:

Ala Arg Arg Met Trp Ala Ser Ala Gin Asn Ile Ser Gly Ala Gly Trp 30 Ser Gly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn 2.025 S Gin Ala Phe Arg Asn Ile Val Asn Met Leu His Gly Val Arg Asp Gly 4.0 Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser Gln Glm Tle Leu Ser Ser 10 65 (2) INFORMATION FOR SEQ ID NO:23: (i) SEQUENCE CHARACTERISTICS: 15 (A) LENGTH: 94 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 20 (ii) WOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23: Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 23 The Arg Ala Gin Ala Gly Leu Deu Glu Ala Glu His Gin Ala Ile Ile 28 Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala 30 Ala Cys Gln Gly Phe Ile Thr Gln Lou Gly Arg Asn Pho Gin Val Ilo 25.45 Tyr Glu Gln Ala Asn Thr His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Xas Ser Ser Trp Ala 35 (2) INFORMATION FOR SEQ ID NO:24: (i) SEQUENCE CHARACTERISTICS: 40 (A) LENGTH: 52 amino acids (B) TYPE: amino scid (C) STRANDEDMESS: single (D) TOPOLOGY: linear 45 (ii) NOUECULE TYPE: peptide (xi) SEQUENCS DESCRIPTION: SEQ ID NO:24: Cly Met Ala Glu Ala Thr Ser Xea Asp Thr Met Thr Glo Met Aso Glo 50 10 Ala Phe Arg Ash Ile Val Ash Met Leu His Gly Val Arg Asp Oly Leu Val Arg Asp Ala Asn Xaa Tyr Glu Gln Gln Glu Gin Ala Ser Gin Gls 55 Ile Leu Ser Ser 50 (2) INFORMATION FOR SEQ ID NO:25:

5		(1)	(A) (B) (C)	358CI L63 TYI STI TO!	ooth 7E: 8 Randi	: 94 Smind SDSR:	ami Sac Ss::	no ad id sing:	ride								
		(ii)	MOL	SCULI	I TYI	PE: 1	pept:	ide									
10		(xi)	382	mac	R DES	CRI	PTIO	S: 31	g n) 180	:25:						
		Met 1	Thr	Ile	Asn	Tyr s	Gln	Phe	Gly	qaa	Val	Asp	Ala	Nis	Gly	Ala 15	Met
15		Me	Arg	Ala	Gln 20	Ala	aly	Ser	žeu	Glu 25	Ala	Ølu	His	Gln	Ala 30	Ile	lle
		Ser	Asp	Val 35	Lessa	Mix	Ala	Ser	Asp 40	Phe	arp	gly	ara	ala 85	GJÀ	Ser	ala
		Ala	Cys 50	Gln	Gly	Phe	lle	Thr 55	Gln	โซน	Sly	Arg	Asn 60	Phe	Gln	Val	Xaa
20		Tyr 65	Glu	Gla	Ala	Asn	Ala 70	His	Oly	eln	Lys	Val 75	Qln	Ala	Ala	aly	Asn So
		Asn	Met	Ala	Gla	Thr 85	Asp	Ser	Ala	Val	Gly 90	Ser	Ser	Trp	Ala		
25	(2)	INFO	emat:	EON 1	POR 1	8 8 Q 3	ID N	0:26:	9								
30		(1) (11)	(A) (B) (C) (D)	STI TOI	KOTH 28: : RAND: POLO:	: 98 imin IONE: IY:]	emi) > ac SS: : Line:	no a: id sing: sr	cids								
35		(ix)		JERCI					BQ II) NO:	:26:						
		Met 1	Thr	Ser	Arg	Phe 5	Met	Thr	Asp	Pro	His 10	Als	Met	Arg	Asp	Met 15	Als
40			Arg	Phe	Glu 20		nis	Ala	Gln	Thr 25		Ølz	qsA	Glu	Ala 30		Āng
		Met	Trp	Ala 35		Als	Gln	Asn	Ile 40		aly	Alæ	Gly	Trp		Gly	Me 0
		Ala	610 50	Ala	Thr	Ser	Leu	Asp 55	Thr	Net	Ala	Gln	Met 60	asa	Gln	Ala	Phe
45		Arg 65	Asn	lle	Val	Asn	Met 70	Leu	Ris	Gly	Val	Arg 75	Asp	Gly	Leu	Val	Arg 80
				Asn	Asn	Tyr 85	Glu	Gln	Gln	Glu	Gln 90	Ala	Ser	Gln	Gln	Ila 95	Leu
50		Ser															
	(2)	INFO															
55		(i)	(A) (B) (C)	JERCI LEI TYI STI	oth: pd:// vandi	: 94 Emina EDME:	ami : 38 C	oo a: (d sing:	ids								

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEC ID NO:27: Š Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 3.0 Tie Arg Ala Xaa Ala Gly Leu Leu Glu Ala Glu Bis Gln Ala Ile Ile 28 Ser Asp Val Lou Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala 10 & Ö Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile 88 Tyr Gin Gin Ala Asn Als His Gly Gin Lys Vel Gin Als Ala Gly Asn 70 75 15 Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala (2) INFORMATION FOR SEQ ID NO:28: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 81 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:28: 30 Arg Phe Glu Val His Ala Gin Thr Val Glu Asp Glu Ala Arg Arg Met Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly Met Ala 28 Xaa Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe Arg 35 **€**♡ Aso Ile Val Aso Met Leu Nie Gly Val Arg Asp Gly Leu Val Arg Asp 55 60 Ala Asn Asn Tyr Glu Glu Glu Glu Glu Ala Ser Glu Glu Ile Leu Ser 40 800 (2) INFORMATION FOR SEQ ID NO:29: (1) SEQUENCE CHARACTERISTICS: 45 (A) LEWGTH: 94 amino acids (B) TYPE: amino acid (C) STRANDEDESSS: single (D) TOPOLOGY: linear 50 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29: Mat Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 55 20 Tie Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile

Ser Asp Val Leu Thr Ala Ser Asp Pho Trp Gly Gly Ala Gly Sor Ala

33 40 Ala Cys Oln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile 55 Tyr Glu Gln Ala Asn Ala Sis Gly Gln Lys Val Gln Ala Ala Gly Asn Š 70 78 Asn Met Ala Gin Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 20 (2) INFORMATION FOR SEQ ID NO:30: 10 (i) SEQUERCE CHARACTERISTICS: (A) LENGTH: 11 amino acids (B) TYPE: amino acid (C) STRAMDEDNESS: single 15 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 20 Gln Glu Gin Ala Ser Gln Gin Ile Leu Ser Ser (2) INFORMATION FOR SEQ ID NO:31: 23 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 94 amino acids (S) TYPE: smino acid (C) STEAMDEDNESS: single (D) TOPOLOGY: linear 30 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31: 35 Mot Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met 10 Ile Arg Ala Gin Ala Gly Leu Leu Siu Ala Giu His Gin Ala Ile Ile 25 Arg Asp Val Leu Thr Ala Ser Asp Phe Trp Oly Gly Ala Gly Ser Ala 40 Ala Cya Gin Gly Phe Ile Thr Gin Leu Gly Arg Asn Phe Gin Val Ile Tyr Glu Gin Ala Asn Ala His Cly Gln Lys Val Gin Ala Ala Gly Asn T045 Asn Met Ala Gin Thr Asp Sor Ala Val Gly Ser Ser Trp Ala (2) INFORMATION FOR SEQ ID NO:32: 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 55 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

		Xet	Ser	Phe	Val	Thr 5	Thr	Gln	Pro	Olu	Ala 10	Leu	Ala	Ala	Ala	Ala 15	Ala
5		Asn	Leu	Gln	30 20	Ile	Gly	Thr	Thr	Net 25	Asn	Als	Gln	Asn	Ala 30	Als	Als
		Als	Ala	Pro 35	Thx:	Titar	Gly	Val	Val 40	Pro	Ala	Ala	Ala	Asy 45	Ølsa	Val	Swr
		Ala	Leu 50	Thr	Ala	Alæ	Sln	Pbe 55	Ala	Ala	His	Bla	eo eo	Met	Tyr	9ln	Thr
10		65	Ser				70					7.8					80
		Val	Ala	Ser	Ser	Gly 85	Ser	Tyx	Ala	Ala	Thr 90	Glu	Als	Ala	Asp	Ala 95	Ala
15		Ala	Ala	Gly													
	(2)	INFO	RMAT	eon i	POR 8	ero :	id w):33	¥								
20		(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 99 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptids															
25	×	(11)	MOL	scuu	z TY)	9E: }	p ep t:	ids									
		(xi) SEQUENCE DESCRIPTION: 88Q ID NO:33:															
30		Met 1	ser	Phe	Val	Thr 5	Thr	Gln	Pro	Clu.	Ala 10	lou	Ala	Ala	Ala	Ala 15	Als
		Asn	beu	Gln	30 30	ric	Gly	Thr	Thr	80et 35	Asn	Ala	Gln	Asn	Ala 30	Ala	Ala
		Ala	Als	Pro 35	Thr	Thr	Gly	Val.	Val 40	Pro	ălæ	Ala	Ala	Asp 45	Glu	Val	Ser
35			Leu S0					55					80				
		65	Ser				70					78					80
40			Als		Sør	Oly 85	Ser	Tyr	Ala	Als	Thr Ş0	Glu	Ala	Ala	Asn	Ala 95	Ala
	2 55 2		ala	······································	N.A.A.	06 000 AO	e ac. 1000										
A &	(2)	info															
45 50		(2)	(B)	. LEI TY: ST:	ngth Pe: (Kand)	: 15 smin: EDNE:	ami: pac: 98: :	no a: id sing:	cids								
w W		(11)	MOL	econ	e TYI	PB:)	pept:	ide									
		(x1)	SEÇ	JENC	s de:	SCRI	PTIO	T: 81	eQ II	o no	:34:						
55		Asp 1	Pno	His	Äla	Met S	årg	Asp	Met	Ala	Gly 10	Arg	Pho	Glu	Val	His 15	
	(2)	info	rmat:	ION I	FOR S	SEQ :	ED N	0:35	ä								

\$		(1)	SEQUENCE CHAI (A) LEMETH: (B) TYPE: 8: (C) STRANDE: (D) TOPOLOG	15 amino mino acid DNESS: si:	acids							
		(11)	MOLECULE TYP	S: peptid	æ							
Ô		(xi)	SEQUENCS DES:	CRIPTION:	ssq m	BO:	35:					
		Arg 1	Asp Met Ala (3ly Arg P S	he Glu	val	Nis 10	Ala	Gln	Thx	Val	Glu 15
Š	(2)	IMFO	MATION FOR S	eq id no:	36:							
0		(1)	SEQUENCE CHA) (A) LENGTH: (B) TYPE: a: (C) STRANDE: (D) TOPCLOG	ls amino mino scid DNESS: si:	acida							
		(ii)	MOLECULE TYP	E: peptid	<u>s</u>							
5		(xi)	SRQUENCE DES	CRIPTION:	ero II) NO:	36:					
		Arg 1	Phe Glu Val :	His Ala G 5	ln Thr	Val	Glu 10	Asp	Gla	Als	grā	Arg 18
0	(5)	IMPO	KATION FOR 8)	EQ ID NO:	37:							
5		(i)	SEQUENCE CHA! {A} LENGTE: {B} TYPE: &! {C} STRANDE! {D} TOPOLOG!	15 amino sico acid CNESS: si	acids							
		(ii)	MOLECULE TYP)	E: peptid	8							
0		(xi)	SEQUENCE DES	CRIPTION:	seo ii) NO:	37:					
		Ala 1	Gln Thr Val (Jlu Asp G S	lu Ala	Arg	Arg 10	Net	Trp	Ala	Ser	Ala 15
5	(2)	INFO	MATION FOR SI	EQ ID NO:	38:							
0		(2)	SEQUENCE CHAI (A) LENGTH: (B) TYPE: a: (C) STRANDE: (D) TOPOLOG!	15 amino mino acid OMESS: si	acids							
		(ii)	MOLECULE TYP:	I: peptid	÷							
5		(xi)	SEQUENCE DES	CRIPTION:	SBQ II) WO:	38:					
		Asp 1	Olu Ala Arg ;	Arg Met T: S	rp Ala	Ser	Ala 10	Gln	Asn	lle	Ser	Gly 15

	(2)	INFO	EMATION FOR SEQ ID NO:39:
5		(1)	SEQUENCE CHARACTERISTICS: {A} LENGTE: 15 amino acids {B} TYPE: smino acid {C} STRANDEDNESS: single {D} TOPOLOGY: linear
10		(i,i)	MOLECULE TYPE: peptide
		(x1)	SEQUENCE DESCRIPTION: SEQ ID NO:39:
15		Met 1	Trp Ala Ser Ala Gln Asn Ile Ser Gly Ala Gly Trp Ser Gly 5 10 15
	(2)	INPO	RMATION FOR SEQ ID NO:40:
20		(1)	SEQUENCE CHARACTERISTICS: {A} LENGTH: 15 amino acids {B} TYPE: amino acid {C} STRANDEDSESS: single {D} TOPOLOGY: linear
25		(11)	MOLECULE TYPE: peptide
		(xi)	SEQUENCE DESCRIPTION: 5%Q ID NO:40:
30		Gln 1	Asn The Ser Gly Ala Gly Trp Ser Gly Met Ala Glu Ala Thr 5 10 15
	(2)	INPO	RMATION FOR SEQ ID NO:41:
35		(\$)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPS: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
40		(ii)	MOLECULE TYPE: peptide
		(x1)	SEQUENCE DESCRIPTION: SEQ ID NO: 61:
45		Als 1	Gly Trp Ser Sly Met Ala Glu Ala Thr Ser Leu Asp Thr Met Thr 5 10 15
	(2)	INFO	RMATION FOR SEQ ID NO: 82:
50		(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids (B) TYPE: smino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
55		(11)	MOLECULE TYPE: peptide
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:42:

Met Ala Glu Ala Thr Ser Leu Asp Thr Met Ala Gln Met Asn Gln 2.0 (2) INFORMATION FOR SEQ ID NO:43: Š. (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 10 {D} TOPOLOGY: linear (ii) MOUNCOUNT TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43: 15 . Ser Leu Asp Thr Met Ala Gln Met Asn Gln Ala Phe Arg Asn Ile (2) INFORMATION FOR SEQ ID NO:64: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 25 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44: 30 Ala Oln Met Asn Glm Ala Phe Arg Asn Ile Val Asn Met Leu His 5 3.0 (2) INFORMATION FOR SEQ ID NO:45: 35 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: smino soid (C) STRANDEDNESS: single 40 (D) TOFOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45: 45 Ala Phe Arg Asn Ile Val Asn Met Leu His Oly Val Arg Asp Cly 10 (2) INFORMATION FOR SEQ ID NO: 46: 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acida (B) TYPE: amino acid (C) STRANDEDNESS: single 55 (D) TOPOLOGY: linear (ii) WOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEC ID NO: 66: Val Asn Met Leu Nis Gly Val Arg Asp Gly Neu Val Arg Asp Als 10 Š (2) INFORMATION FOR SEC ID NO:47: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 10 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47: Gly Val Arg Asp Gly Leu Val Arg Asp Ala Aso Aso Tyr Glu Glo 10 . 15 20 (2) INFORMATION FOR SEQ ID NO:48: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 25 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptids 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48: Leu Val Arg Asp Ala Asn Asn Tyr Glu Gln Gln Glu Gln Ala Ser 35 (2) INFORMATION FOR SEQ ID NO:49: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids 40 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) NOWECOUR TYPE: peptide 45(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49: Asn Asn Tyr Glu Gin Gin Giu Gin Ala Ser Gin Gin Ile Leu Ser Ser 3.0 50 (2) INFORMATION FOR SEQ ID NO:50: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 17 amino acids 55 (8) TYPE: amino acid (C) STRANDEDMESS: single (D) TOFOLOGY: linear

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50: 3 Met Ala Ser Arg Phe Met Thr Asp Pro Ris Ala Met Arg Asp Met Ala Gly (2) INFORMATION FOR SEQ ID NO:51: 10 (i) SEQUENCE CERRACTERISTICS: (A) LENGTE: 15 amino acids (B) TYPS: amino acid (C) STRANDEDNESS: single 15 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51: 20 Met Thr Ile Asn Tyr Oln Phe Gly Asp Val Asp Ala His Gly Ala 3.0 (2) INFORMATION FOR SEQ ID NO:52: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 30 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52: 35 Gln Fhe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Glo 1.0 (2) INFORMATION FOR SEQ ID NO:53: 488 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids (B) TYPE: amino acid (C) STRANDEDNESS: single 45 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:53: 50 Asp Ala Mis Gly Ala Met Ile Arg Ala Gln Ala Ala Ser Leu Glu 8 (2) INFORMATION FOR SEQ ID NO:54: 55 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (S) TYPE: amino acid

(C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 4 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54: Met Ile Arg Ala Cln Ala Ala Ser Lew Glu Ala Glu His Gln Ala 3.33 10 (2) INFORMATION FOR SEQ ID NO:55: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids 15 (%) TYPE: amino acid (C) STRAMDEDMESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 20 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55: Ala Ala Ser Leu Glu Ala Glu Ris Gln Ala Ile Val Arg Asp Val 25 (2) INFORMATION FOR SEQ ID NO:56: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 30 (B) TYPE: amino acid (C) STRANDEDSESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 33 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56: Ala Glu Mis Gln Ala Ile Val Arg Asp Val Len Ala Ala Gly Asp 10 40 (2) INFORMATION FOR SEQ ID NO:57: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acida (B) TYPE: amino acid 45 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 50 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57: Tie Val Arg Asp Val Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala 5 35 (2) INFORMATION FOR SEQ ID NO:58: (i) SEQUENCE CHARACTERISTICS:

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(A) LEMOTH: 16 amino acids
               (8) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
5
         (ii) MOLECULE TYPE: peptide
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:
10
          Leu Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln
                                              3.0
     (2) INFORMATION FOR SEQ ID NO:59:
15
          (i) sequence characteristics:
               (A) LENGTH: 15 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
20
         (ii) WOLECULE TYPE: peptids
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:
25
          Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu Phe lie Thr
      (2) INFORMATION FOR SEQ ID NO:60:
30
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 15 amino acids
               (B) TYPE: amino acid . .
               (C) STRANDEDWESS: single
               (D) TOPOLOGY: linear
35
         (ii) MOLECULE TYPE: peptide
         {xi} SEQUENCE DESCRIPTION: SEQ ID NO:60:
40
          Gly Ser Val Ala Cye Gln Glu Phe lie Thr Gln Leu Gly Arg Asn
                                              3.0
     (2) INFORMATION FOR SEQ ID NO:61:
$5
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 18 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDWESS: single
               (D) TOPOLOGY: linear
50
         (ii) MOLECULE TYPE: peptide
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:
55
          Gin Glu Phe Ile Thr Gin Leu Gly Arg Asn Pho Gin Val Ilo Tyr Glu
                                              10
          Gin Ala
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	(2)	INFOR	NATION FOR SEQ ID NO:62:
5		(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: line&r
10		(11)	MOLECULE TYPE: peptide
			SEQUENCE DESCRIPTION: SEQ ID NO:62:
15		Arg	Asn Phe Gln Val Tle Tyr Glu Gln Ala Asn Ala His Gly Gln 5 10 13
• •	(2)	INFO	RMATION FOR SEQ ID NO:63:
20		(1)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
25		(11)	MOLECULE TYPE: peptide
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO.63:
30		lle 1	Tyr Glu Gln Ala Asn Ala Ris Gly Gln bys Val Gln Ala Ala 5 10 15
	(2)	INFO	RMATION FOR SEQ ID NO:64:
35		(i.)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linsar
40		(ii)	MODECOLE TYPE: paptide
		(xi)	SEQUENCE DESCRIPTION: SEQ ID NO:64:
4 5		Asn 1	Als His Cly Cln Lys Val Cln Ala Ala Cly Asn Asn Met Ala 5 10 15
	(2)	INFO	WATION FOR SEQ ID NO:65:
50		(3)	SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
S5		(ii)	MODECTUE TYPE: peptide
			SEQUENCE DESCRIPTION: SEQ ID NO:65:
		Earnes	all and and after all all days and and after all all after that

3. 10 15 (2) INFORMATION FOR SEC ID NO:66: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 10 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66: 15 Gly Asn Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala 3.0 (2) INFORMATION FOR SEQ ID NO:67: 20 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPS: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 25 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 67: 30 Asp Ala His Gly Ala Met Ile Arg Ala Leu Ala Cly Leu Leu Glu (2) INFORMATION FOR SEC ID NO:68: (i) sequence characteristics: 33 (A) LENGTH: 15 amino scide (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 40 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68: 45 Asp als His Cly Ala Met Ile Arg Ala Sin Ala Gly Leu Leu Glu 8 1 (2) INFORMATION FOR SEQ ID NO:69: 50 (i) SEQUENCE CHARACTERISTICS: (A) LEWOTH: 15 smino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 55 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Met lie Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala 10 (2) INFORMATION FOR SEQ ID NO:70: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid 10 (C) STRANDEDERSS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70: Met lie Arg Ala Gin Ala Gly Leu Leu Glu Ala Glu His Gin Ala 23 20 (2) INFORMATION FOR SEQ ID NO:71: (i) SEQUENCE CHARACTERISTICS: (A) LENGTE: 15 amino acids (B) TYPE: amino acid 25 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71: Ala Oly Leu Leu Clu Ala Olu His Gln Ala Ile Ile Ser Asp Val 35 (2) INFORMATION FOR SEQ ID NO:72: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid 40 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 45 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72: Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile Arg Asp Val 50 (2) INFORMATION FOR SEQ ID NO:73: (i) SEQUENCE CRARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: smino acid 55 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

		(x1)	SECUE	NCE DE	SCRI)	PTIO	: SE	Q II) NG:	:73:					
5		Ala 1	Slu H	is Gln	Ala 5	Ile	Ils	Ser	Asp	Val 10	Leu	Thr	Ala	ser	Asp 15
	(2)	INFOR	OITAM	I FOR	SRQ :	m w	8:74:								
10		(i)	(B) (C) (C)	ICE CE LENGTH TYPS: STRAND TOPOLO	: 15 amin EDNE:	ami: > ec: 89: :	to ac .d :ingl	ids							
15		(11)	MOLECU	ILE TY	PE: 3	pepti	ide								
		(xi.)	SEÇUE	FCE DE	SCRI	PTIOS	: SE	O II	NO:	74:					
20		Als l	Glu Hi	is Gln	Ala S	ĭls	Ile	årg	Asp	Val 10	Les	Thr	Als	Ser	Asp 15
	(2)	INFOR	CHATION	FOR .	ero :	ed M	3:75:								
25		(1)	(B) 7 (C) 8	ics ch Jength Typs: Ftrand Topolo	: 15 emina EDNE:	ami: > aci 35: :	o sc id singl	ìás							
30		(11)	MOLECU	ile tr	PE:)	ept.i	de								
		(xi)	SEQUE	FCE DE	9CRI)	PTIO	r se	Q II	2 100	75:					
35		Ile 1	Tle Se	er Asp	Val 5	Leu	Thr	Ala	Sex	Asp 10	Phe	Trp	Gly	Gly	Alx 15
	(2)	INPOS	(MATIO	FOR:	SSQ :	m ci):76;								
\$ 0		{ £}	(B) 1 (C) 8	ice ch Jenoth Type: Itrabo Topolo	: 15 amino EDNE:	amir aci 88: 8	io ac .d :ingl	ids							
45		(ii)	MOLECU	TLE TY	PE: g	epti	.de								
		(xi)	SEQUES	ice de	SCRII	PTION	: SS	Q II	100	76:					
50		110 1	Ile Ar	rg Asp	Val 5	Leu	Thr	Ala	Ser	Asp 10	Phe	Txp	Gly	Gly	Ala 15
	(3)	INFOR	MATION	for :	seo :	id nc	777;								
55		(1)	(8) 1 (C) s	ICB CR JENGTH TYPE: : TRAND	: 16 amino EDNE:	amir > aci !8: s	o ac d ingl	ids							

(ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77: 5 Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln 3.0 (3) INFORMATION FOR SEQ ID NO:78: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: smino scid (C) STRANDEDNESS: single 15 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78: 20 Phe Trp Gly Gly Ala Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr (3) INFORMATION FOR SEQ ID NO:79: 25 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino scid (C) STRANDEDNESS: single 30 {D} TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79: 35 Gly Ser Ala Ala Cys Gln Gly Phe Ile Thr Gin Leo Gly Arg Asn (2) INFORMATION FOR SEQ ID NO:86: 40 (i) SEQUENCE CHREACTERISTICS: (A) LENGTH: 15 amino acids (8) TYPS: amino acid (C) STRANDEDNESS: single 45 (D) TOPOLOGY: linear (ii) WOLBCULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80: 50 Gin Gly Phe Ils Thr Gin Leu Gly Arg Asn Phe Gin Val Ile Tyr (2) INFORMATION FOR SEQ ID NO:81: 55 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 25 smino acids (B) TYPE: smino acid

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(C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
         (ii) MOLECULE TYPE: peptide
 5
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:
         Val Thr Thr Asn Phe Phe Cly Val Asn Thr Ils Pro Ils Ala Leu Asn
                                     3.0
10
          Glu Ala Asp Tyr Leu Arg Met Trp Ile
                     20
     (2) INFORMATION FOR SEQ ID NO:82:
15
          (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 25 amino scids
               (B) TYPE: smino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
20
         (ii) MOLECULE TYPE: peptide
         (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:
25
         Asn Glu Ala Asp Tyr Leu Arg Met Trp Ile Gln Ala Ala Thr Val Met
          Ser His Tyr Glm Ala Val Ala His Glu
30
     (2) INFORMATION FOR SEQ ID NO:83:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 967 base pairs
              (B) TYPE: nucleic acid
35
              (C) STRANDEDMESS: single
              (D) TOPOLOGY: linear
           (ii) MOLECULE TYPE: cDNA
40
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:
     TGAGCCCCAA CCCTACCGTC GGTTCGTCAC ACGGACCGCA TGGCCTGCTC CGCGGACTGC
                                                                           80
     CGCIAGGGTC GCGGATCACT CGGCGTAGCG GCGCCTTTGC CCACCGATAT GGGTTCCGTC
                                                                           3.20
     ACACTETOST TECCOSCOCO CCATOSSCOS GATAACGCCA TGACCPCAGC TOSSCAGAA
                                                                           180
35
     TRACABTROT COCABARROR TRARCACCOR BARRACABOTA ARCARCART CRINTECOST
                                                                           240
     TTGTSACTAC CCAACCAGAA GCACTSGOOG COGCGGCCGG CAGTCTGCAG GGAATCXGCT
                                                                           300
     COSCATTGAA COCCCAGAAT GOGGCTGCCGG CGACTCCCAC GACGGGGGTG GTCCGGCGGC
                                                                           360
     CECCGATUAA NTGTCGGCGC TGACGGCGGC TCAGTTCGCG GCACACGCCC AGATCTATCA
     SECOSTCAGO GOCCAGGOOG CEGOSATTOA OGAGATETTO GTCAACACTO TACAGATGAG - 480
50
     CTCASSSTOS TATSCTECTA CCSASSCOSC CAACSOSSCC GCSGCCSSNT AGASSAGTCA
     CTGCGATGGA TTTTGGGGGCG TTGCCGCCGG AGGTCAATTC GGTGCGGATG TATGCCGTTC
     CTESCTCGC ACCAATSSTC SCTGCGGCGT CCCCCTGGAA CGGGTGGGCC GCGGAGCYGA
                                                                           560
     STTOSSCORT CACCOSTTAT GAGACOSTGA TCACTCAGCT CASCASTGAG GGGTGGCTAS
     OTCOSCOTO ADOSCOATO GCCGASCOAS TTGCGCCOTA TETGCCGTSG ATGASTSCOG
                                                                           780
33
     CTGCGGCGCA AGCCGAGCAG GCGGCCACAC AGGCCAGGGC CGCCGCGGCC GCTTTTGAGG
                                                                           640
     COSCITTEC COCCACGOTS CCTCCCCCT TGATCSCCGC CAACCGGGCT TCGTTGATGC
                                                                          900
     ASCIDATOTO GACGAATGIC TITGGICAGA ACACCICGGC GATGGCGGCC GCCGAAGCIC
                                                                          960
     AGTACGG
                                                                           267
```

	{2} INFORMATION FOR SEQ ID NC:84:
Ś	(i) SEQUENCE CHARACTERISTICS: {A} LENGTH: 15 amino acids (B) TYPS: amino acid (C) STRANDEGNESS: single (D) TOPOLOGY: linear
10	(ii) MOLECULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:
15	Met Ser Phe Val Thr Thr Sln Pro Slu Ala Asau Ala Ala Ala 1 5 10 18
	(2) INFORMATION FOR SEQ ID NO:85:
20	(i) SEQUENCE CHARACTERISTICS; (A) LENGTH: 15 aming acids (B) TYPE: aming acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
25	(ii) MOLECOLE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:
30	Thr Oin Pro Glu Ala Leu Ala Ala Ala Ala Asa Leu Oln Gly 1 5 10 15
	(2) IMPORMATION FOR SEQ ID NO:86;
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (8) TYP8: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
40	(ii) MOLECULE TYPE: peptide
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:86:
45	Lou Ala Ala Ala Ala Aon Lou Gln Gly Ile Gly Thr Thr Met i 5 10 15
	(2) INFORMATION FOR SEQ ID NO:87:
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (S) TYPE: smino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear
55	(ii) MOLSCULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

Als Asn Leu Gin Gly lie Gly Thr Thr Met Asn Als Gin Asn Als (2) INFORMATION FOR SEQ ID NO:88: 3 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 smino acids (S) TYPE: amino acid (C) STRANDEDNESS: single 30 (0) TOPOLOGY: Linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88; 35 Ile Gly Thr Thr Wet Asn Ala Gln Asn Ala Ala Ala Ala Pro 18 (2) INFORMATION FOR SEQ ID NO:89: 20 (i) SEQUENCE CHARACTERISTICS: (A) LEWGTH: 15 amino acids (8) TYPE: amino acid (C) STRANDEDNESS: single 25 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89: 30 Asn Ala Gln Asn Ala Ala Ala Ala Ala Pro Thr Thr Gly Val Val (2) INFORMATION FOR SEQ ID NO:90: 33 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single 40 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30: 45 Ala Ala Ala Ala Pro Thr Thr Gly Val Val Pro Ala Ala Ala Asp (2) INFORMATION FOR SEQ ID NO:91: 50 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 smino scids (8) TYPE: amino acid (C) STRANDEDNESS: single 55 (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91: Thr Thr Gly Val Val Pro Ala Ala Ala Asp Glu Val Ser Ala Seu 1.0 3 (2) INFORMATION FOR SEQ ID NO:92: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids 10 (%) TYPE: smino sold (C) STRANDSONESS: single (b) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 15 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92: Pro Ala Ala Ala Asp Glu Val Ser Ala Leu Thr Ala Ala Gln Phe 20 (2) INFORMATION FOR SEQ ID NO:93: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 25 (B) TYPE: amino acid (C) STRANDSDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 30 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93: Glu Val Ser Ala Leu Thr Ala Ala Gln Phe Ala Ala His Ala Gln \$ 3. 10 35 (2) INFORMATION FOR SEQ ID NO:94: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 smine acids 40 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide \$5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94: Thr Ala Ala Gln Phe Ala Ala His Ala Gln Set Tyr Gln Thr Yal 50 (2) INFORMATION FOR SEC ID NO:95: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids 33 (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide (xi) sequence description: SEQ ID NO:95: 5 Ala Ala His Ala Gin Met Tyr Gin Thr Val Ser Ala Gin Ala Ala 3.0 95 (2) INPORMATION FOR SEQ ID NO:98: 10 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 16 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 15 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96: 20Met Tyr Glo Thr Val Ser Als Glo Ala Ala Als Ile Sis Glu Met Phe (2) INFORMATION FOR SEQ ID NO:97: 23 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 30 (ii) MOLECULE TYPE: peptide (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97: 35 Ser Ala Gin Ala Ala Ala Tie His Giu Met Phe Val Asn Thr Leu \$5.7 2.0 3. (2) INFORMATION FOR SEQ ID NO:98: 40 (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids (B) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: linear 45 (ii) WOLECULE TYPE: peptide (xi) SECUENCE DESCRIPTION: SEO ID NO:98: 50 Ala Ile His Glu Met Phe Val Asn Thr Leu Val Ala Ser Ser Gly (2) INFORMATION FOR SEQ ID NO:99: 55 (1) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEONESS: single

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(D) TOPOLOGY: Linear
            (ii) MOLECULE TYPE: peptide
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:
      Phe Val Asn Thr Leu Val Als Ser Sor Gly Ser Tyr Ala Ala Thr
10
    (2) INFORMATION FOR SEQ ID NO:100:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 15 amino acids
              (B) TYPE: amino acid
15
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: peptide
20
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:
      Val Ala Ser Ser Cly Ser Tyr Ala Ala Thr Clu Ala Ala Asn Ala
25
     (2) INFORMATION FOR SEQ ID MO:101:
            (i) SHOUENCE CHARACTERISTICS:
              (A) LENGTH: 14 amino scids
              (B) TYPE: amino acid
30
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: peptide
33
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:101:
      Ser Tyr Ala Ala Thr Glu Ala Ala Ass Ala Ala Ala Gly
      3
40
     (2) INFORMATION FOR SEQ ID NO:102:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1764 base pairs
              (B) TYPE: nucleic acid
45
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
            (11) MOLECULE TYPE: CDMA
533
     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:102:
     ATTOGTTCCT GCCGCAGCTA AATCCCGGGG ACATCGTCGC CGGCCAGTAC GAGGTCAAAG
     GCTGCATCGC GCACGGCGGA CTGGGCTGGA TCTACCTCGC TCTCGACCGC AATGTCAACG
     GCCGTCCGGT GGTGCTCAAG GGCCTGGTGC ATTCCGGTGA TGCCGAAGGG CAGGCAATGG
                                                                           180
55
     CSATGSCOGA ACGCCAGTTC CTGGCCGAGG TGGTGCACCC GTCGATCGTG CAGATCTTCA
                                                                           240
     ACTITICES OCACACCIAC ACCCACOSSIG ATCOSSITOS CIACATOSIG ATGGAATACS
                                                                           300
     TOSSOSSIA ATOSOTOAAA COCASCAASS STOANAAACT SCOOTOSOS GAGGOCATOS
                                                                         360
     CCTACCTGCT GGAGATCCTG CCGGCGCTGA GCTACCTGCA TYCCATOGGC TYGGTCTACA
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ACGACCIGAA GCCGGAAAAC ATCATOCTGA CCGAGGAACA GCTCAAGCTG ATCGACCTGG
      GCGCGSTATC GCGGATCAAC TCGTTCGGCT ACCTCTACGG GACCCCAGGC TTCCAGGCGC 540
      CCSAGATOST GCGGACCEST CCGACGGTGG CUACCGACAT CTACACCTTG GGACGCACSC
      TUGOUGUGUT CACGUDGAC CTGCUCACCO GCAATGGCCG TTATOTOGAT GGGCTACCCG
     AAGACGACCC GGTGCTGAAA ACCTACGACT CTTACOGCCG GTTGCTGCGC AGGGCCATCG 720
      ACCCCGATCC GCGGCAACGG TTCACCACCG CCGAAGAGAT GTCCGCGCAA TTGACGGCCG
      TSTTGCGGGA GGTGGTCCCC CAGACACCGG GGTGCCGCGG CCAGGCTATC AACGATCTTC
     AGTCCCAGTC GGTCGACATT TGGAGTGGAC TGCTGGTGGC GCACACCGAC GTGTATCTGG 900
     ADSSCREET SCACECORS ASSCREACES CCAACSASAT OFTGACECO CTGTORSTSC
10
      COCTOSTOGA TOUGACUSAC STOSCASCII COSTOCTOCA GOCCACGGIO CICTOCIAGO 1830
      COGTECAGAC CCTAGACTCS NTSCGCGCGC CCCSCCACGG TGCGCTGGAC GCCGACGGCS 1090
      TOSATINICO GAGICAGIGG AGCIGCOCT AAIGGAAGIC CGCGCGCTGC ISGAICICEG 1140
      CGATGTGGCC AASGCCACCC GAAAACTCGA CGATCTGGCC GAACGCGTTG GCTGGCGATG 1200
      SCRATTGGTC TGGTACCGOG CCSTCGCCGA GCTGCTCACC GGCGACTATG ACTCGGCCAC 1260
15
     CARACATTE ACCGAGGIGC TERRITACCIT TOCCGGCGAG CIGGCGCCA AGCICGCCCI 1320
     SGCCGCCACC GCCGAACTAG CCGGCAACAC CGACGAACAC AAGTTCTATC AGACGGTGTG 1300
     GAGCACCAAC GACGGCGTGA TCTCGGCGGC TTTCGGGACTG GCCAGAGCCC GGTCGGCCGA 1440
     AGGTGATCGG GTCGGCGCCG TGCGCACGCT CGACGAGGTA CCGCCCACTT CTCGGCATTT 1500
     CACCACGGCA CGGCTGACCA GCGCGGTGAC TCTGTTGTCC GGCCGGTCAA CGAGTGAAGT 1560
     CACCEAGGAA CAGATCOBOG ACECCCCCO AAGAGTOGAG ECCCTGCCCC CGACCGAACC 1620
20
     ACROSTGCTS CAGATCCGCS CCCT8GTSCT GGGTGCCCCC CTGGACTGGC TGAAGGACAA 1680
     CAAGGCCAGC ACCAACCACA TOCTOGGTTT COCOTTCACC AGTCAONGGC TOCGGCTGGG 1740
     TUTCHAGGCG TUACTGCGCA GCCTGGCCCG GGTAGCTCCC ACTC
                                                                        3784
25
     (2) INFORMATION FOR SEQ ID NO:103:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 766 base pairs
              (B) TYPE: mucleic acid
30
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
            (ii) MODECULE TYPE: CONA
35
            (xi) SEQUENCE DESCRIPTION: SEO ID NO:103:
     ACAARACACT CGGYGGCKGC COMTCCGGCC TGATCGTGGG TGATCAGCYT CGTGCCAAAY
     TODGCACAG GTGCGCGCTE CCCAANGAGT TCTTCGCCGC RGTGCGMGCM KAACTGGCCT
                                                                        120
     ATCNTGGTTG GGTGCCGTCC CGCAMAACCC GCGACTTAA ACCCATTTTA ACCGGGCAGG
                                                                        180
40
     AASTITICITA CATYTACCON RESHAWCCAA COSSGCCSCC NANAAMTCOS TOCTOSANTO 240
     CGANCGOTTC COMPTOTTOG COGCACTGCT GACCGGCACG GARTATCCGC AGGCGGCGTT 306
     OCCCAACOCO TOCOTOCAAC TOCCCTACGG TGCGCACCAS GACGCCATCA CCGGCTCGGA 360
     GICCGACCAG GIACTCAATG CYGGCGACCA CACTAGCCAG CAGACCAAAC IGTIGCAGGC 420
     CGATUTOCAS GOGOGOGOGO COGGTGGCAT ACGGATTXOT CGAAACCAAT COGGAGGAAT 480
45
     TCATCACGGA COUTCACOGA AAACGATCGC CCCAATGGIN GGACNACCCN AGCCAGGGIN 540
     ATTWACCOIT MAACAACITG GNGTAGGITC TITGATATCG AKCAACCGAT ACGGAKOGGM 600
     CCGCGGAATG GTAGACCACC ACCAGTOCCC NCANCINGIG CACCAGTITG GTCATCCCCC - 550
     SCAGATOGGT GACCCCGCCA ASCSTTCCGG ATSCSSAGAT GASGCTQACC AGCCYGGTTG 720
     ACCIVITIGAT CAGGITIFICE CAGRECIACS TEGOCASETS SECSET
                                                                         756
50
     (2) INFORMATION FOR SEQ IS NO:104:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1231 base pairs
55
              (B) TYPE: nucleic soid
             (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
```

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(ii) WOLECULE TYPE: cDWA
            (xi) SECURNCE DESCRIPTION: SEC ID NO:104:
      CGCCACGAGA ATTICGCCTG TGCCTCGATA GCCACTTGCC TGTDGTCGCG CTGCCAGCGG
      STUAGUUAGG TUGUUTGUTU CAGGULATUG GOUUGGUGUA GGAGGGUGAT GTTSGULAGA
                                                                        120
      CCCGGTTTAC GAGAACCGGA CTCTACNAAG TGTCGGCGCT GACGGCGGCT CAGTTCGCGG
                                                                        180
      CACACECCCA GATCTATCAS GCCGTCAGCG CCCASGCCGC GGCGATTCAC GAGATGTTCG 240
      TCAACACTCT ACAGATNANC TCAGGGTCGT ATSCTGCTAC CGAGGCCGCC AACGCGGCCG 300
10
     COOCCOCTA GARGASTCAC TOCGATOCAT TTTOOGGCGT TGCCGCCGGA GGTCAATTCG 380
     STECRENTET ATECRETCE TESCTCEGEA CCAATEGICS CIGCEGEGIC GOCCTEGAAC
     GGGTTGGCCG CGGAGCTGAG TTCGGCSGCC ACCGGTTATG AGACGGTGAT CACTCAGCTC
     ASCASTGAGG GGTSSCTAGG TCCGGCGTCA SCSSCGATGG CCGAGGCAGT TGCGCCGTAT 540
      GTOGCOTOGA TRAGTGCCGC TOCOGCGCAA GCCGAGCAGG CGGCCACACA GGCCAGGGCC
                                                                        600
15
     GCCGCGGCCG CTTTGAGGC GGCGTTTGCC GCGACGGTGC CTCCGCCGTT GATCGCGGCC
                                                                        660
      AACCOGGCTT COTTGATGCA GCTGATCTCG ACGAATGTCT TTOOTCAGAA CACCTCGGCG 720
     ATCGCGGCCG CCGAAGCTCA GTACGGCGAG ATGTGGGCCC AAGACTCCGC GGCGATGTAT
                                                                        780
     OCCTACOCOO OCAOTTOGOC GASCOCCTOS OCOSTCACOC COTTTAGCAC OCCGCCGCAS
                                                                        840
     ATTGCCAACC CGACCGCTCA GGSTACGCAG GCCGCGGCGG TSGCCACCGC CGCCGGTACC
                                                                        900
     GCCCAGTCGA COCYGACGGA GATGATCACC GGGCTACCCA ACGCGTGCA AAGCCTCACC
20
                                                                        360
     TURCHICTET TOCAGTOSTO TRACEGICOS CIGITOSTOSO TETOGORASAT CITETICOSO
                                                                        1020
     ACSCCCAATT TOOCCACCTC AATTTOGGCA CTGCTGACCG ACCTGCAGCC CTACGCGAGC
     TINTINTATA ACACCGAGGG CCTGCCGTAC TICAGCATCG GCATGGGCAA CAACTICATT
                                                                        1140
      CASTOGGOCA AGACCOTGGG ATTGATOGGC TAGGOGGCAC CGGCTGCGGT CGCGGNTGCT
                                                                        1200
25
     GGGGATNCCG CCAAGGGCTT GCCTCGTGCC G
                                                                        1231
     (2) INFORMATION FOR SEC ID NO:105:
            (i) SEQUENCE CHARACTERISTICS:
30
             (A) LENGTH: 2041 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
35
           (ii) MOLECULE TYPE: cDNA
            (xi) SEQUENCE DESCRIPTION: SEO ID NO:105:
     CGGCACGAGC TCGTGCDGAT CAGTGCCATT GACGGCTTGT ACGACCTTCT GGGGATTGGA
40
     ATACCEAACC AACGOGGTAT CETTTACTCC TCACTAGAGT ACTTCGAAAA AGCCCTGGAG
                                                                       120
     GAGCTGGCAG CASCGTTTCC GGGTGATGGC TGGTTAGGTT CGGCCGCGGA CAAATACGCC 180
     GBCAAAAACC GCAACCACGT GAATTTTTTC CAGGAACTGG CAGACCTCGA TCGTCAGCTC
                                                                       240
     ATCAGCCTGA TCCACGACCA GGCCAACCCG GTCCAGACGA CCCGCGACAT CCTGGAGGGC 300
     SCCAAGAAG GTCTCGAGTT CSTGCCCCC GTGGCTGTGG ACCTGACCTA CATCCCGGTC 360
45
     OTCHOGCACO CCCTATCOCC COCCTTCCAN GCGCCGTTTT GCGCGGGGGC GATGGCCTTA 420
     GTOGGOGGG CGCTTGCCTA CTTOGTCGTG AAAACGCTGA TCAACGCGAC TCAACTCCTC
                                                                        480
     AAATTGCTTG CCAAATTGGC GGAGTTGGTC GCGGCCGCCA TTGCGGACAT CATTTCGGAT 540
     OTOSCOGACA TCATCAAGGG CATCCTODGA GAAGTOTOGC ADTTCATCAC AAACGCGCTC 600
     AACGGCCTGA AAGAGCTTTG GGACAAGCTC ACGGGGTGGGG TGACCGGACT GTTCTCTCGA 660
50
     GGGTGGTGGA ACCTGGAGTC CTTCTTTGG GGGGTCGCG GGTGACGG GGGGACCAGC
                                                                        720
     COCTIVICAC AASTGACTAG CITATICAGI GCOGCOGGIC TETCCGCAIC GTOGGCTIG
                                                                        780
     CONCACSOS ATACOMES CASCIDASC ASCITSCOS CONTECÇÕE CATIGEGES 840
     GGGTCCGGTT TTGGGGGCCTT GCCGAGCCTG GCTCAGGTCC ATGCCGCCTC AACTCGGCAG 900
     GCGCTALGGC CCCGAGCTGA TROCCCGGTC GGCGCCGCTG CCGAGCAGGT CGGCGGCAG
33
     TOGCAGCIEG TOTOCOGUCA GEGITOCCAA GETATUGGCG GACCCGTAGG CATGGGCGGC
     ATSCACCCCT CTTCGGGGGC GTCGAAAGGG ACGACGA AGAAGTACTC GGAAGGCGCG 1080
```

GOGGOGGCA CTGAAGACGC CGAGCGCGCGC CCAGTCGAAG CTGACGCGGG CGGTGGGCAA

ARGETGCTEG TACEARACET CETCTARCEG CATGGCGAGC CARATCCATT GCTAGGCAGC 1200

1140

```
GCCTAACAAC GCGCAATGCT AAACGGAAGG GACACGATCA ATGACGGAAA ACTTGACGGT
      CCASCCCGAG COTCTCGGTG TACTGGCGTC GCACCATGAC AACOCGGCGG TCGATGCTTC 1120
      CTCGGGCGTC GAAGCTGCCG CTGGCCTAGG CGAATCTGTG GCGATCACTC ACGGTCCGTA 1280
      CTECTCACAS TICAACGACA COTTAAATSI STACTIGACT SCCCACAATS CCCTSSSCIIC 1440
 ş
      STECTIGEAT ACGGCOSTS TOGATCICC CAAAAGICIT CGAATTGCGG CGAAGATATA 1500
      TAGGGAMBOC GACGAAGGGT GOCGCAAGGC TATCGACGGG TTOTTTACCT GACCACGTTT 1880
      GCTGCCCGCA GTGCAGGCCA CGACGTAGCG CAGGTCGTGT CCCTCGTAGG CDTGGATGCG 1620
      ACCESCOASC ACCASCACCO GETSCSCACC GATGGSCACG GACAGTASCT CGCCCGCATG 1880
      CCCGGCTGCG GTTGGCBGCA CAAACCCGGG CAGTTCGGCC TGCGGCAGCA CGGTGGTMGG 1746
10
      GGASCCCARC GCCGCAACGG CCCGTAACCA TCCCGACCCG AGCACGACCG AGACGTCATG 1800
      TTCSCCGATC CCGGTGCGGT CAGCGATGAC CTGCGCCGCCC CGCCGGCCCA GTTTGTCGGG 1850
     ATCOGGOCO GOTCASCCA CACTOGOCOA SCTTAACTOA GCCCCTCOCC GGGAGCGGG 1920
      TGCTNGTCGA TGAGATACTG CGAGCATGCC AGCAGCCAGC GCATCCGAGCA GCGTCGAGGA 1980
      ATTESTGCGC CGCCGTGGTG GCGAGCTGTT CGAGCTGTCC CATGCCATCC ACCTCGTTCC
                                                                                  2040
15
                                                                                  2041
     (2) INFORMATION FOR SEQ ID NO:186:
             (i) SEQUENCE CHARACTERISTICS:
20
               (A) LENGTH: 1202 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDMESS: single
               (D) TOPOLOGY: linear
25
             (ii) MOLECULE TYPE: cDNA
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:106:
      GAGCTCACCO CTATCAACCA ATACTTTCTO CACTCCAAGA TGCAGGACAA CTGGGGTTTT
30.
      ACCEAGOTES CESCOCACAO COSOSCEGAS TOSTOCACES AAATSOSGCA CECOCAGGAA
                                                                                   120
      ATCACCGATC GCATCTTGTT GCTGGATGGT TTGCCGAACT ACCAGCGCAT CUGTTCGTTG
      COTATCOGCC AGACGCTCOS CGAGCAATTT GAGGCCGATC TGGCGATCGA ATACGACGTG
      TYVAATCUTT TCAAGCCAGO AATCUTCATU TUCCEGGAGA AACAGGACAC CACCAGCECC
                                                                                   300
      GTACTGCTGG AGAAAATCGT TGCCGACGAG GAAGAACACA TCGACTACTT GGAAACGCAG
CTGGAGCTGA TGGACAAGCT AGGAGAGGAG CTTTACTCGG CGCAGTGCGT CTCTCGGCCCA
35
      COGACCTGAT GCCCGCTTGA GGATTCTCCG ATACCACTCC G880GCGCGCT GACAAGCTCT AGCATCGACT CGAACAGCGAC TGGGAGGGGG GATATGGCGG GCCCACAGC ACCGACCACT GCCCCCACCG CAATCCGAGC CGGTGGCCGG CTGCTCAGTC CGGTGGGACG CAACATTATT TTCACCGCAC TTGTGTTCGG GGTGCTGGTC GCTGCGACCG GCCAAACCAT CGTTGTGCCC
                                                                                  480
                                                                                  600
      TTCACCOCAC TTOTOTTCOO GOTGCTGGTC GUNGUACUG UCUARUM
GCATTGCCGA CGATCOTCGC CGAGCTGGGC AGCACCOTTG ACCAGTCGTG GGCGGTCACC
                                                                                  880
40
                                                                                   720
                                                                                   780
      TOWCCOCAA CAGGGTGCTG CTAGGCTCCG TCGTGGTCTT CGTCGTTGGC TCTGTGGCTGT
                                                                                  840
                                                                                900
      GCGGGTTATC GCAGACGATG ACCATGCTGG CGARCTCTCG CGCACTGCAG GGCGTCGGTG
      COSSTSCIAT TTCCSTCACC OCCTACSCIC TOSCCSCTSA GSTGGTCCCA CTGCSGGACC
                                                                                  980
45
      GTGGCCGCTA CCAGGGCGTC TTANGTGCGG TGTTCDGTGT CAACACGGTC ACCGGTCCGC 1020
      TUCTUGGGGG CTGCCTCACC GACTATCTGA GCTGGCGGTG GGCGTTCCGA CCACCAGCCC 1080
      CATTACCGAC CCGATCGCGG TCATCGCGGC GAACACCGCC CTCGCGGGCGT TGCGGGCAGG 1140
      TCCCTTGGG AACGTGGTCC CACAGCGCCA GAACGGTCGG AAATGCGATG GCCGACCTAC 1200
                                                                                  1202
50
     (2) INFORMATION FOR SEC ID NO:107:
             (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 496 base pairs
55
               (B) TYPE: mucleic scid
               (C) STRANDEDNESS: single
```

(D) TOPOLOGY: linear

```
(11) MOLECULE TYPE: CONA
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:107:
 5
     SSCHAARDAA COASRECTT SECORATES SOESSRITES ACCUSED ACCUSED
     CCTEGGCAG CAGCCEGGAC CECGNACCET GATCAGTING GATCGCCGGG ACCGCCGCCG 120
     ACCAANGOTA TTCCGCCCRT GARGAAGTCG GAANTRIGCG CAGIGATGAC GCCCTGCTGC 180
     AACGENTOCE GEATTGCTGA GEGGATOSCE GEOGGAAOGGE GGTGCTCACE ACCEGGGGGGC 240
     ACCCCTACRE ACASSCCCSC ATASCTGAAT SACSCCGGGT NACCGCCGTC CCNTCCACCS 300
10
     EGANATOGC CCGGANGCAA AAGATOCSTC GGCGCTCCGC CTCGGCGACG ACAGCCACGT 360
     TCACCCGCGC GTTATCGGTG GCCGCGATCS CATACCAGGC GCCGTCAAGG TMGCCGTYGC
     GGTAGTCACG CACCGACAAG GTGATYTSGT CCATCGCCTN GACGGCGGGG GTGACGCTGG
                                                                         480
     GGGCGATCAM GTGCAC
                                                                         496
15
     (2) INFORMATION FOR SEQ ID NO:108:
            (i) SECUENCE CHARACTERISTICS:
             (A) LEMOTH: 849 base pairs
             (B) TYPE: nucleic acid
20
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
           (11) MOLECULE TYPE: CONA
25
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:108:
     TSSATTCCCA TACCOGTTTC GSCCCCTCGA CGGCGACCA CGGCGCGCGCAG GCCTCCGAAC
     GGGGGGCCGG GACGCTGGGA TTCGCCGGGA CCGCAACCAA AGAACGCCGG GTCCGGGCGG 120
     TOGGGCTGAC CNCACTGGCC GGTGATGAGT TCGGCAACGG CCCCGGGATG CCGATGGTGC 180
30
     CEEGGACOTO GRASCAGOO DOCASCAGACO COSACEGATOS GEGASCAGO
     GAGGCGACGG CTTACCGCAC GACAGCAAGT AACCGAATTC CGAATCACGT GGACCCGTAC 300
     OCCTOGRARG GRORGATOTT ATGROCCTTT TOGRTGCTCR TRTCCCRCRG TYCOTGGCCT 360
     CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCGGCA CACGATCGGT CAGGCCGAGC 420
     ASSCRICTANT GTCSGCTCAS GCGTTTCACC AGGGGGAGTC GTCSGCGGGG TTTCAGGCCG 480
     CCCATGCCCG GTTTGTGGCG GCGGCCGCCA AASTCAACAC CTTGTTGGAT GTCGCGCAGG 540
35
     CSAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTGCGGCC GCGTCGACCT 600
     ATACONGOYY CYGAYCGAAC CCTGCTGACC GAGAGGACTY GTGAYGYCGC AAATCAYGYA 660
     CAACTACCCC GCGATGTTGG GTCACGCCGG GGATATGGCC GGATATGCCG GCACGCTGCA
                                                                        720
     CASCITIGOT OCOGAGATOS OCSIGEROCA OGCOGOSTIS CAGASICOST GOCAGGOGGA
                                                                        780
40
     TACCEGEATO ACGTATORGE COTOGORGEO ACANTESTAR CORNECORNE GRAGATITISS
                                                                         840
     TOCGGGCCT
                                                                         849
     (2) INFORMATION FOR SEQ ID NO:109:
45
            (1) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 97 smino acids
             (B) TYPE: amino acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
50
           (ii) MOLECULE TYPE: protein
           (xi) SECURNCE DESCRIPTION: SEC ID NO:109:
55
     Met Ser Leu Leu Asp Als Ris Ils Pro Gin Leu Val Ala Ser Gin Ser
      3
                                     10
     Ala Phe Ala Ala Lys Ala Gly Leu Wet Arg His Thr Ile Gly Gln Ala
```

2.5

	Glu	Øln	Ala 35	Ala	Net	Ser	Ala	01m 40	Ala	Phe	His	Gln	Gly 45	Glu	Ser	Ser
	Ala	Ala 50		Gln	Ala	Ala	His 55		Arg	Phe	Val	Ala 60		Ala	Ala	Lys
5	Val 65		Thr	Leu	Leu	Asp 70		Ala	Gln	Ala	Asn 78		sly	Olu	Ala	Ala 80
		Thr	Тух	Val	Ala 85	Ala	qaA	Ala	Ala	Als 90	Als	Sex	Thr	Tyx	Thr 95	Gly
10	Phe															
	(2)	Inpoi	RMAT:	ION :	FOR 8	e Çer	id m):11(3 \$							
15		(:	(A) (B) (C)	EQUEI LEN(TYP: STRI TOP(ITH: I: ac Andsi	15 a sino DNES:	mino acid 3: s:	o aci i ingle	ids							
20			ii) i	MOLE	TULE	TYP	ğ: 308	eptic	ie							
		(I	ki) i	SEQUI	SNCS	DESC	RIP	fion:	: SE(gi ç	11 CM	110:				
25	Not 1	Ser	Leu	Leu	Asp S	Ala	His	ïle	Pro	Oln 10	leu	Val	Ala	Ser	91n 15	
	(2)	Infoi	emat)	ION I	FOR S	EQ :	ID NO	3:113	l :							
30		· Ç:	(A) (B) (C)	eque: Lenc Typi Stee Topo	fik: 1: an Woel	15 x mino MES	min: acid : si	o aci i ingle	ids							
35		£ 2	ii) t	40LE(TULE	TYPE	i pe	sptić	ie							
		(3	ki) 8	e r Qui	ence	DESC	iripi	TION:	88() ID	NO:1	lll:				
40	Ala 1	His	Ile	Pro	Gln 5	Leu	Val	Ala	Ser	Gin 10	Ser	Ala	Phe	Ala	Ala 15	
	(2)	INFO	rmat)	ion i	FOR S	8 8 Q 3	D 80	0:222	1							
45		(2	(A) (B) (C)	eque: Lenc Typ; STR; Top(fik: 1: ac Mori	15 a siso XXBSS	umine ació }: \$i	o aci ingle	ದೆತ							
50		()	ii) »	401.BC	:ULS	TYPE	i: ps	ptić	le							
		(3	xi) 8	FRQUE	ince	DSS	RIP	non:	SMC	in	NO :)	112:				
3 5	Leu 1 (2)			Ser ION P	8					Als 10	Lys	Ala	Gly	Leu	Net 18	
		13	() gre	arstaten	smas n	*27% % *	Section 2015	e al estables	ുനമും							

```
(A) LENGTH: 15 amino acids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
 5
            (ii) MOLECULE TYPE: peptide
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:113:
10
      Ser Als Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly
     (2) INFORMATION FOR SEQ ID NO:114:
15
            (i) SEQUENCE CHARACTERISTICS:
              (A) LEMCTH: 15 amino acids
              (B) TYPE: amino acid
              (C) STRANDEDWESS: single
              (D) TOPOLOGY: linear
20
            (ii) MOLECULE TYPE: peptide
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:114:
25
      Lys Ala Sly Leu Met Arg His Thr Ile Cly Sln Ala Glu Gln Ala
       1
                       83
     (2) IMFORMATION FOR SEQ ID NO:115:
30
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 15 amino scids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
35
            (ii) MOLECULE TYPE: peptide
            (%1) SECURNCE DESCRIPTION: SEC ID NO:115:
40
     Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala Met Ser Ala Gln
   (2) INFORMATION FOR SEQ ID NO:116:
45
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 15 smino acids
              (B) TYPE: amino acid
              (C) STRANDEDNESS: single
              (D) TOPOLOGY: linear
50
            (ii) MOLECULE TYPE: peptide
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:116:
35
     Gin Ala Glu Gin Ala Ala Met Ser Ala Gin Ala Phe Ris Gin Gly
     (2) INFORMATION FOR SEQ ID NO:117:
```

(i) SEOURNCE CHARACTERISTICS: (A) LEMOTH: 15 amino acids (8) TYPE: amino acid 5 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:117: Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala 1.0 15 (2) INFORMATION FOR SEQ ID NO:118: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino soid 20 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:118: Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln Ala Ala His 3. 85 30 (2) IMPORMATION FOR SEQ ID NO:119: (i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids (B) TYPE: amino acid 35 (C) STRANDEDNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: pentide 40 (wi) SEQUENCE DESCRIPTION: SEQ ID NO:119: Glu Ser Ser Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala 45 (2) INFORMATION FOR SEQ ID NO:120: (i) SEQUENCE CHARACTERISTICS: (A) LEMOTH: 15 smine acids (8) TYPE: amino acid 50 (C) STRANDEUNESS: single (D) TOPOLOGY: linear (ii) MOLECULE TYPE: peptide 55 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:120: Phe Gin Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val 20

	(2) INFORMATION FOR SEQ ID NO:121:
5	(i) BEQUENCE CHARACTERISTICS: {A} LENGIN: 15 amino acids {B} TYPE: amino acid {C} STRANDEDNESS: single {D} TOPOLOGY: linear
10	(ii) MOLECULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:121:
15	Ala Arg Phe Val Ala Ala Ala Ala Lys Val Asn Thr Lev Leu Asp 1 5 10 15
	(2) INFORMATION FOR SEQ IS NO: 122:
20	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino acids (B) TYPE: amino acid (C) STRANDEDNESS: aingle (D) TOPOLOGY: linear
25	(ii) MOLECULE TYPE: peptide
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:122:
30	Ala Ala Ala Lys Val Asn Thr Leu Leu Asp Val Ala Gin Ala Asn 1 5 15
	(2) INPORMATION FOR SEQ ID MO:123:
35	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: 15 amino scids (8) TYPE: amino acid (C) STRANDEDNESS: single (D) TOPOLOGY: Linear
40	(ii) NOLECULE TYPE: peptide
	(xi) sequence description: seq id no:123:
45	Asn Thr Leu Leu Asp Val Ala Gin Ala Asn Leu Gly Glu Ala Ala 1 10 15
	(2) INFORMATION FOR SEQ ID NO:324:
50	(i) SEQUENCE CHARACTERISTICS: (A) LENGTH: l8 amino acids (B) TYPE: amino acid (C) STRANDEDMESS: single (D) TOPOLOGY: linear
55	(ii) MOLSCULE TYPE: peptide
	Cod 5 commons mariner morning come to section a.

```
Val Ala Oln Ala Asn Leu Gly Clu Ala Ala Gly Thr Tyr Val Ala Ala
      1
      Asp Ala
 5
     (2) INFORMATION FOR SHO ID NO:125:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 1752 base pairs
              (B) TYPE: nucleic acid
10
              (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
            (ii) MOLECULE TYPE: cDMA
15
           (xi) SEQUENCE DESCRIPTION: SEQ ID No:125:
      COGCACGAGA ATGTCGCCTG TGCCTCGATA GCCACTTGCG TGTGGTCGCG CTGCCAGCGG
      STCAGCCAGG TOTOTOTO CAEGOCATO STCAGOCAGG GGAGCGCTAT GTTGCCAGA
                                                                         120
      CCCGGTGTAC GAGAACCGGA CTCGACNAAG TGTCGGCGCT GACGGCGGCT CAGTTCGCGG
                                                                         2.80
20
     CACACGCCCA GATCFATCAS GCCGTCAGGG CCCAGGCCGC GGCGATTCAC GAGATGTTCG
                                                                          240
     TCAACACTCT ACAGATNANC TCAGGGTCGT ATGCTGCTAC CGAGGCCGCC AACGCGGCCG
                                                                         300
     COGCCGGCTA GAGGAGTCAC TGCGATGGAT TTTGGGGCGT TGCCGCCGGA GOTCAATTCG
                                                                         360
     GTGCGGATGT ATGCCGGTCC TOGCTCGGCA CCAATGGTCG CTGCGGCGTC GGCCTGGAAC
      GOSTTOSCCS COGRACTGRO TYCGGCSSCC ACCOSTYRYG AGRCGGTGRY CRCYCRGCTC
                                                                         480
     AGCAGTGAGG GGTGGCTAGG TCCGGCGTCA GCGGCGATGG CCGAGGCAGT TGCGCCGTAT
25
     OTTOCCTOGA TGAGTOCCOC TGCGGCGCAA GCCGAGCAGG CGGCCACACA GGCCAGGCCC
     GCCGCGGCCG CTTTTGAGGC GGCGTTTGCC GCGACGGTGC CTCCGCCGTT GATCGCGGCC
     AACCGGGCTT CGTTGATGCA GCTGATCTCG ACGAATGTCT TTDGTCAGAA CACCTCGGCG
     ATCGCGGCCG CCGAAGCTCA GTACGGCGAG ATGT99GCCC AAGACTCCGC GGCGATGTAT
30
     GCCTACGCGG GCAGTTCGGC GAGCGCCTCG GCGGTCACGC CGTTTAGCAC GCCGCCCCAG
     ATTGCCAACC CGACCGCTCA GGGTACGCAG GCCGCGGCGCGC TGGCCACCGC CGCCGGTACC
     GCCCASTUBA CECTGACEGA GATGATUACC GGCCTACCCA ACGUSCTGCA AAGCCTCACC
     TCACWTCTGT TGCAGTCGTC TAACGGTCCG CTGTCGTGGC TGTGGCAGAT CTTGTTCGGC 1070
     ACCCCCAATT TCCCCACCTC AATTTCCCCA CTGCTGACCC ACCTGCACCC CTACGCGACC 1080
35
     TINTINTATA ACACCGAGGG CCTGCCGTAC TTCAGCATCG GCATGGGCAA CAACTTCATT 1140
     CASTUDGOCA AGACCOTOSS ATTGATCOSC TASSOCISCAC COSCUSCOST OSCOSCUSCUS 1200
     SCHEATECCS CCAAGGCCTT SCCTBEACTS GGCGGGATGC TCGGTGGCGG GCCGGTGGCG - 1260
     SCOSSICTOS SCAATGESSE TICGGITGSE AAGCISTOGG TECCSCOSSI SIGGABIGGA 1320
     COSTUCCOS COTOCOSTOAC TOCOMOGOCT COTOCOCTAC COSTUACIAC GOTOACTUCO 1380
40
     GCCCCGGAGG COSCCCCGG AAGCCTGTTS GGCGGCCTGC CGCTANCTOS TSCGGGCGGG 1440
     SCCSSCSOGS GTCCACGCTA CSGATTCCRT CCCACCSTCA TSSCTCGCCC ACCCTTCSMC 1500
     GOGATAGTCG CTGCCGCAAC GTATTAACGC GCCGGCCTCG GCTGGTGTGG TCCGCTGCGG 1560
     STESCAATE STENGESCES AAATSTESST SSSTATTTE OSSTOSSATT TITTECSSAA 1620
     GCCGGGTTCA REACCGGATT TCCTAACGGT CCCGCKACTC TCGTGCCGGA TTCGGCACTA 1680
45
     ASTGACGICC GGCGGAAACC CUITGGGINT GAAAGCTICA GAAAGCCCG CICCCAGGGG 1740
     TTCGGCAAAC GG
                                                                         1752
     (2) INFORMATION FOR SEQ ID NO:126:
50
           (i) SEQUENCE CHARACTERISTICS:
              (A) LEWSTH: 400 smino acids
              (B) TYPE: amino acid
             (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
55
           (ii) MOLECULE TYPE: protein
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:126:
```

	Met 1	Asp	Phe	Gly	Ala S	Leu	Pro	Pro	Glu	Val	Asn	Ser	Val	Arg	Met 15	Tyr
5		gly	Pro	@ly 20	Ser	Als	Pro	Wet	Val 25		ala	Ala	Ser	Ala 30		Ass
	Gly	Leu	Ala 35		Glu	Leu	Ser	Ser 40		Als	Thr	Gly	Tyr 45	Glu	Thr	Val
	Tle	Thr 50	Gla	Leu	Ser	Ser	Giu SS	Gly	Trp	Leu	Gly	Pro 60	Ala	Ser	Als	Als
10	Met 65	Ala	Glu	Ala	Val	Ala 78	Pro	Tyr	Val	Ala	Trp 75	Met	Ser	Ala	Ala	Alz 80
	Ala	Ola	Ala	Glu	Gln SS	Ala	Ala	Thr	Gln	Ala So	Arg	Ala	Ala	Als	Ala 95	Ala
15	Phe	Glu	Ala	Ala 100	Phe	Ala	Ala	Thr	Val 105	Pro	Pro	Pro	Lou	lle 110	Ala	Alæ
	Asn	Arg	Als 113	ser	I/834	Met	Gln	1.20	Ile	Sex	Thr	Asn	Val 125	ədq	Gly	Gla
	Asa	Thr 130	Ser	Ala	Ile	Ala	Als 135	Als	Glu	Ala	Gln	Tyr 140	Gly	Glu	Met	Trp
20	Ala 145	Glm	Asp	Sar	Ala	Ala 150	Met	TYE	Ala	Tyr	Als 155	Gly	Ser	Ser	Ala	80r
	Ala	Ser	ala	val	Thr 165	Pro	Phe	Ser	Thr	Pro 170	Pro	Gln	lle	Ala	Asn 175	Pro
25				180	Thr				1.85					130	-	
	Ala	Cln	30r 195	Thr	beu	Thr	Glu	Met 200	Ilæ	Thr	Gly	Leu	Pro 295	ABB	ala	Leu
		210			Ser		235					220	-			
30	338				Ile	230					235					340
					Thr 245					280					288	
35				280	pro				285					270		
			275		Tha			280					285			
1.00		290			Gly		29%					300				
40	395			••	•	310				•	315					Ser 320
					325 325					330					335	
45				340					245					350		Ala
			355		Ala			360					365			
82.50		370			ala		375					380				
50	Val 385	Met	Ala	Arg	Pro	9ro	Phe	xaa	Cly	lle	Val 395	Ala	Ala	Ala	Thr	Tyr 400
	(2)	infoi	emat)	CON 1	FOR S	e cae	ED 186):121	7 s							

(i) SEQUENCE CHARACTERISTICS:

55

- (A) LENGTH: 474 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single

```
(D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: cDNA
 5
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:127:
       GGCACGAGCA CCAGTTEACC CGCGAAGAAC CTEACCSCGC CACCCAGCGC CGCCGCATC
       ACCESCOCCE TOCCACGAAC CTTTTCGSTA AACGAGCCAC TCCASCGGAG ATCGGTACCG 120
       CCCGACGCAT TTGGTGTAAG GACCACCTCG CCGAAGTAGT CCTGGACGGG TGTCCTCGCG 180
10
       CCAACCAGCT TSTAGACETG GCGACGTTCC TGCTCATACT CGACGGTCTC TTCCTGCACG 240
       AACACCGGCC ACATGCTAG TTTGCGGATG GCCCCGATGC CGCCGGGCGC GGGATCACCG 300
       CGTCGCGCCC AACTCGATTG AGCAACGATG GGCTT00CCC AGGTCGCCCA GTTGCCACCG 360
       TCTGTCACGA GCCGAAACAA GCTTGCAGCC GGCGCGCTGC TGGTCTTGGT GACCTCGAAC 420
       GAAAATTYCC GACCGGACAT GCGCGACTCC CGAAACGACA ACTGAAGCTC GTGC
15
      (2) INFORMATION FOR SEQ ID NO:128:
               (i) SEQUENCE CHARACTERISTICS:
                 (A) LENGTH: 1431 base pairs
20
                 (B) TYPE: mucleic soid
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear
              ((i) MOLECULE TYPE: CONA
25.
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:128:
       CT9C9C9CCG GAAAAANTA TTACT99CRG GACCGGCAGA AT9CAT99TG ATATTCCGGT
       GATGAGGCCG CCGAGGAACC GACTAGTGCG AQGGTCAACA CATCGGTTAT TCGTTGCCGT
                                                                                            120
       TTAGGTCTTG GATCTGCCGG GACGGCAACG AGTTGGCAGG ACCGCTCACG CGAGCGCTGT 180
30
       TGACAGAGIC GOTTCACOTC GAACTCGCCA CCCGTCAGAT GCGAATGATA GCCACATCGG 240
       CCACACCATC GACGGGGTCG AAGTCGCCGT CGTGGGTCAC GACCGGCACC CCTTGCGACG
                                                                                           3.00
       TOGCAACAGC AGCGGCCCTC ACCGGACGGG ACCGAGATCG TCGGTGGTGT CGCCAGTGAG 360
       CGTTGCGAGG TCGCGGGTGC AATCCCGCAT CTGCTTGCGT ATGCCGAAGC CGCCGCAGCA
GCTCGTCTCG ACTCAACCAT CGGCGCCGTG CGGGCTGCCT GCGGTCAGCA GCGCAACCGG
35
      GCTCSTCTCG ACTCAACCAT COSCSCCSTS CSSGCTGCCT GCSSTCASCA GCSCAACGGG 480
TTTGCCGTTG GCAGTSATSG TGATGTCTTC GCCSSCCTGC ACGCGCCGTA GCAGCCCGGC 540
GGTGTTGTTG CGCAGTTCGC GAGACGCGAC TTCAGCAGGC ATGCTGCGGG GATCGGCTTG 600
CGCTGGGCGC GGTGTCACCG TCATGCGCTT GGGATATCAC GTGATCTATC GGCACGAAGC 660
CGCCGGATGA GCGAGGCAA CCGCCTACAC GGGCTGCCTC GCCTTGACCG CGCCGAACGT 720
TACTGTGCCG GGGGCATCAG CACCGTATCG ATCATGTACA CCGTCGCGGG GGCGCACGTATGA
CTCCGCCCACA TACCAAACAG GACGTGTTGA CCATGAGTCG TCGCGGGCGC CACCACCT 840
40
       CASSICSCA COTTSCASGI CIGATOGGIO COSTOSATOO ISCICSGACI COCCISSCOS
       SCHATCACUT SCHASSICAS SATSCHSCHS AGCASCITOS COTCASTCHT GASTHSATCS
       ATASTEGOCO COGGCAGCTT GTCEAATECE GCETTGGTGG GGGCGAAAAC GGTGTACTCS 1020
45
       CCGCCGTTGA GGGTGTCGAC CAGATTCACA TCCGGGTTCA GCTTGCCCGA CAGAGCCGAG 1050
GTCAGGGTAC TGAGCATCGG GTTGTTGGAA GCCGCGGTAG CGACCGGGTC TTGCGCCATT 1140
       CCGGCCACCE ATCCGGGACC GGTGGGATTT TECGGCGGGT ATTGCGCGGCA CCCACGACCA 1200
                                                                                        1260
       ATCAGGTCCG CTGCGGTCAG CCATTGCCGC CGTGGTAACG GGCGCCGCCG GGCTGGTCGC
       COSTITIONS CIGGROUNT COSACACOS TITOSTOCIC SAACACCOS CIAASAACSC 1320
50.
      AATOSCGATG OCTGCGAGGC TCGCTGCTGC GGCCGGTTTG GCCTGAACGT TGATCATCGC 1380
       TTCGATTCCT TTGCTTCTGC GGCGGCGTTG AACGCCGTCC TCCTGGGTRG A
                                                                                          1431
      (2) INFORMATION FOR SEQ ID NO:129:
55
               (i) sequence characteristics:
                 (A) LENGTH: 279 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS; single
```

```
(D) YOPOLOGY: linear
             (ii) MOLECULE TYPE: CDMA
 5
             (xi) SECUENCE DESCRIPTION: SEC ID NO:129:
      GCACCAGAGT COTATCTTTC CACCAGCOC COSTAGGARA COGCTGGCCT GGCTAACTCA
      GATGOGGGGG GCCGTCGATT CGAGAGGTAA CCGATCGCCC GCCGACAATG GGTTACCCAC 120
      CRAGACTGAT TGCCGCGCAG CCGCCTTCGA CGTGTAAGCG CCGGTTCGTG CATGCCCGGA 180
10
      ACCCCCCAC TCACCCACCT TCTACCTACT ACCTCACCCA CTTTTACCCA TTATOCCCCA
                                                                                  240
      CONTETTEC CICCCAGGAC ICCAGAATCI ACTOSTGCC
                                                                                  279
      (2) INFORMATION FOR SEQ ID NO:130:
15
             (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 1470 base pairs
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
20
             (ii) MOLECULE TYPE: CDNA
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:130:
25
      ACCECCACCC GCAGCCEGA ATCACCETTE GTAACCTECG AATACAATTT CTTCATCGAC 🦾 60
      CACTTOOGGA ACAGCGAACC CGAGCCCACC GCCTGATAGC CTTCTTCCTC GATGTTCCAA
                                                                                  130
      COCCCGCCC COTCGAACGA AACGATACGA CCCCCCCTCT GCGGGTCAGA CGCATGAATG
                                                                                  1.80
      TOGTAGOCCO CCASCAACOS CAACOCCASC AGACOCTISCA TOGOSGOCGO CAGATTISCOA
                                                                                  240
      COCACCATAA TCCCCACCO GTTSATTTTS CCCGCAAACG TCAGCGGCAC ACCCTCGAGC
                                                                                 300
      TTCTCGTAGT GCTCAAGTTC CACGGCATAC AGCCGGGCAA ACTCAACCGC GACCGCAGCC 360
30
      OTOCCAGORA TOCCOGOTAGO GOTOTAGTOA TOCGOTOATAT ACACOTTOCO CACATCACOC
                                                                                  420
      CCAGAAATCA TGTTGCCCTAC CGTCGAACGC CGGTCACCCG CCATGACAAC ACCGCCGGGG 480
TATTTCAGCG CGACAATGGT GGTGCCGTGC GGCAGTTGCG CATGACCAC ACCGCCGGGGGGGC 540
GCACCGCCGC TGATGCTTGC CGGCAGCAAC TCCGGGGGCGCA GAAGTCAAGT 600
GAAAGAAGAT AGGTCTACAG CGGGTGTTCC AGAGAGTGAA TTAATGGACA GGCGATCGGG 660
CSACCGCCGC GTTAATGTTTCC GCGTTTTTGG ACTGTATGTCC GGACGAAGTC CTCTGCTTTC 736
35
      CAACOGCCAG GTCACTOTCC GCCCTTTTGG ACGTATGCGC GGACGAAGTC CTCGGCGTTC
      TECTOGRAGGA COTOGROGAT TYCGTCGRGC AGATEGYCGG TETECTEGGT CACCTTYTEG 780
      CGACSCTCCT GGCCCGCGGC GGTGCTGCCG GCGATGTCGT CATCATCGGC GCCGCCACCG 940
      CCACOCTTGG TOTOCTCTTG COCCATCOCC GCCTCCTGCT TCCTCATGGC CTTTCAAAAG 900
40
      SCCSOSSGTS COCCECTACAC SCCCSCTSTC TTTCTCTCAC CTACCAGTCA ACACCAACST
                                                                                 960
      TTCCCBBCCT AACCABBCTT ABCBAGGCTC ABCBBTCAGT TSCTCTACCA GCTCCACBGC
                                                                                 1020
      ACTOTOCACO GAATOCAGCA ACGCACCAAC ATGCGCCTTA CTACCCCGCA ACGGCTCCAG 1980
      CGTCGGGATG CGAACCAGCG AGTCGCCGCC AGGTCGAAGA TCACCGAGTC CCAGCTAGCC 1140
      GUGGURATAT CAGCCCCGAA CCGGCGCAGG CATTTCGCCG CGGARATACG CGCGGGTGTC 1200
45
      COTCOCCOOT TUTCUACUCC ACTCACCACC TOSTSTTTCS STSACTARAC SOTTIATUSA 1250
      SCCGCGCGCG ACCAGCCGGT TOTACAGGCC CTTGTCCAGC CGGACATCGG AGTACTGCAG 1320
      GTTGACGAGG TOCAGCOGG GCCCCGACCA OCTCAGGTTC TCCCGCTGCC GGAAACCGTC 1390
      GASCASCOSC AGITTISGCCS SCCAGICCAG CASCICCSCS CAATCVAICS GSICACGCIC 1440
      GASCISATEC AGCACGTGTG CCCAGGTTTC
                                                                                 1470
50
     (2) INFORMATION FOR SEQ ID NO:131:
             (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 1059 base pairs
55
               (B) TYPE: nucleic acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
```

```
(ii) MOLECULE TYPE: CONA
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:131:
     ATTCCCATCS CTCCSSCACC TATCACCAGS TAGTCGGTTT CSATGGTTTT CGCCGGCCCT
      TOCOTTOCCC TOCOCCACOO OTCOTTCATO COCCUTCCTG TSCQGATTGG AATTTOTGAC 120
     AACGAAATCG GGCGATCGGT GAGCAATCGT CGCCGATGCA AGACACGCTT TCGCTGCCGC 180
     GECGTCAGGT GGAGTTTAGG CCAGCGTAAC AACGTAGACC GECCACTGAC CAAACCCCAA
     ACCCACAAAC CCTGGACGCA THOGGGTCTC GGGCDTCAAA TTCCGGGTAG ATATCCTATA
10
     COSATATOGO ATSCOOTASC CITATOSASS CATSAGACSC COSCTAGACO CACSGGATAT
     TUCAGATGAS CTOCOGOSAC SECTESSECT CTTOSATGCS GTGGTSATCS GGCTTSGGTC 420
      CATGATCEGY GOUGGRAFOT TEGCTOFFEC CERRITORSC REGRECTOFF GOUGRAFTEG 480
      GCACGAGATT CCAATCCCCA GAAGGTCGTA CAAGCCGTCA ATGGCACTTG ATCGTTGGAT 540
      COATGATGAA COCTCTGCTC ATGCCTGCCC CCTATCTCAA COCTCGTCGA TTCCATGCAT 600
15.
     TAGCCTTGGT TCTGCATTGC ACCCGTAGGG CCTACAGTCT GGCTGTCATG CTTGGCCGAT 660
     CTCAACAGTT TITTTCATCC TAAGCAGATC GTCAGTTTTG AGTTCGTGAA GACGGCATGT 720
      TCACTTETTO TOBACTACAT COTOTOGOCA CATTTOCOCT COTGCAACTO CÓCTGOGACA
                                                                         780
     ATGOSCURAC COCCOTOTAS CTCOTOCOSA ATTOSSCACO AGGATCUACO GGACATESCO
     GACGACTACG ACGAGGCCTG GATGCTCAAC ACCGTGTTCG ACTATCACAA CGAGAACGCA
                                                                         900
     AAAGAAGAGG TCATCYATCT COTGCCCGAC GTGAACAAGG AGAGGGGGCC CATCGAACTC
20
     GTAACCAAGG TAGACAAAGA GOGACATCAG ACTOOTCTAC GATGGGGAGC CACGTTTTCA 1020
     TACAAGGAAC ATCCTAAGTT TTGATTCGGG AACATCCTA
                                                                         3.050
     (2) INFORMATION FOR SEQ ID NO:132:
25
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 153 base pairs
              (B) TYPE: nucleic acid
             (C) STRANDEDNESS: single
30
             (D) TOPOLOGY: linear
           (ii) MOLECULE TYPE: cDNA
            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:132:
35
     SCACGAGGCA TTGGCGGGCA TCTGCATAAA CGGTGACGTA TCAGCACAAA ACAGCGGAGA
     CAACAACATG CGATCAGAAC GTCTCCGGTG GCTGGTAGCC GCAGAAGGTC CGTTCGCCTC
                                                                          3.20
     GOYGTATTIC GACGACICGC ACGACICGTG CCG
                                                                          3.53
40
     (2) INFORMATION FOR SEQ ID NO:133:
            (i) SEQUENCE CHARACTERISTICS:
              (A) LENGTH: 387 base pairs
              (B) TYPE: nucleic scid
$5
              (C) STRANDEDNESS: single
             (D) TOPOLOGY: linear
           (ii) MOLECULE TYPE: coma
50
           (xi) SEQUENCE DESCRIPTION: SEQ ID NO:133:
     COSCSCERTO GATCACCGAS CCASSCAAAA ACTOCSTOSA GCCCGAGTOO ATGATESTCA
                                                                         80
     CCCGGCGCAG CATCTGGCGA ACGATCACCT CGATGTGCTT GTCGTGGGTC GACACACCTT
                                                                          3.30
     OCCONCROTA CACCTCOTEC ACCTORDEAA CCACGTSTAT CTECACCTCC CGGGGGCCCT 180
55
     SCACCCGCAS CACCTCATEC SECTCCCCCS ASCCTTCCAT CAECTSCTES CCCACCTCCA 240
     CETGETOGIC ATOGGAGAGC ACCOETTIGG AACOETCITO GYGCTTGAAC ACCOGCAGCI
                                                                         300
     SCTSCCCTT GEAGATCTTS TOSTAGACCA CTTCCTCACC SCCSTCSTCA GEAACGATGG 360
     TUATCITUTA GAACCGCTCG CCGTCCT
                                                                         387
```

	(2) INFORMATION FOR SEQ ID NO:134:	
5	(1) SEQUENCE CHARACTERISTICS: (A) LENGIH: 389 base pairs (B) TYPE: nucleic acid (C) STRANDEONESS: single (D) TOPOLOGY: linear	
10	(ii) MOLECULE TYPE: COMA	
	(x1) SEQUENCE DESCRIPTION: SEQ ID NO:134:	
15	GTTCAGCACE GCTATCCGAT TUTGCCGTTC GCTTCGGTGG GTGCTGAACA CGGCATCGAC ATCGTGCTCG ACAACGAATC CCCACTGCTG GCACCGGTCC AGTTCCTCGC CGAGAAGCTG CTCGGCACCA AAGACGGTCC GGCGCTGGTC CGTGGTGTCG GACTGACACC GGTACCGCGC CCCGAACGGC AGTATTACTG GTTCGGCGAG CCAACCGACA CCACAGAGTT TATUGGGCAG	50 120 180 240
20	CAAGCCGACE ATAACGCCEC ACGCAGGGTS CGCGAGCGTG CCGCCGCCGC TATCGAACAC GGCATUGAGC TGATGCTGGC CGAGCGCGCA GCCGATCCAA ATCGATCCCT GGTCGGACGG CTCTTGCGCT CGGACGCCTA AGGCGCCCC	300 360 389
	{2} INFORMATION FOR SEQ ID NO:135:	
25	(i) SEQUENCE CHARACTERISTICS: {A} LENGTH: 480 base pairs {B} TYPE: nucleic acid {C} STRANDEDNESS: single {D} TOPOLOGY: linear	
30	(ii) MOLECULE TYPE: CDMA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:135:	
35	CCCCOCOTCG GAATGATCCC COTCTCGTCG COCGCCCATT TGATGCTGTT GATGAGCTGT TTOGAGAAGC CCGGTTGGCG TACCCGTUAG CCGGAATATC TGTTUGAAGC GTCACCGGAT GTMCACATGA ANTNCHTTON CCCHGTMGCG GTNTTGGNTG MGGMAAACAC GTGTTGTYTA AGCCTTGNTG GNCTCGNAAG NGCCGTBGAC GCCTGTGTCG CCGAAGATAA TGAGCACCTG ACCGTTGGCG GGATCGCCGT TATCCCAAGG AATTCCGAGG TCGGTCCCGG AGATGCCGAA	60 120 180 240 300
40	GOSTTOCAGG GTCTTGTTGG GGCTSTCCGG TCOGGTCACC CACTGGGGGA GGGATGTGGN AGCCCGGGG AGCGTGGCAC CAGGATCCGG CGCCGCGCC GGAGCAGGGT CGGNNSCTGN	360 420
46	NCTENNITCC INENGCCHAA TINNACICCN NCNACAANCI IGMNNCCGAC ICHWACCOSH	480
	(2) INFORMATION FOR SEQ ID NO:136:	
45	(i) SEQUENCE CHARACTERISTICS: {A} LENGTH: S87 base pairs {B} TYPE: nucleic acid {C} STRABDEDNESS: single {D} TOPOLOGY: linesr	
50	(ii) MOLECULE TYPE: COMA	
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:136:	
55	GCACGAGGCT ACCGGCGCGT CGCCCGCCAT GCCCTGGATG CACGCGTAGC CACCCGINCA THCAGCGGGT CAGCCGCCGC GTCCGGGCTT AACGCTATAG CAGCTGCAAA CAACCCAGCG CCGGCAATTA CTTTGATGTT GAACCGATGA CCAINGCCTN CGNGTNCAAT CTCNTCTCTT NGCGCGCCGC TAITINNGCC ATANATYTGG TINNANNCON AACGCTAGAC GTAICGAGTT	60 120 180 240

```
CCTTTTCGAC CACCOGCTCA ATTOTCASCA TCCTATGGGG AACATGAGCC CCGCGGCACC
       SUSCEPTITE CAAATSSISA COITCACAACS SISTEACAAS CEAGESCAAT SICESSISTA 360
       GGGACGCGGC GGCTGGGATC GGTGGGGTGA GCGCCCGGCT TCTCAAAGCG AGGGGAGCCC
       CESCACTOTT ACCESCOGAA GEOGGOGGGT GTCACTGATC TAGGOTGAGG GCCAGYNGGT
       GHTNAGCCAA CAAGGATGAC NACAAATAAN CCGAGGANAG ACANGHGACG GNCCGANANG 540
       CTWANCEGON NITTONECNAA MENACNCAC IINTACCOME CITATON
                                                                                         587
      (2) INFORMATION FOR SEQ ID NO:137:
10
              (i) SEQUENCE CHARACTERISTICS:
                (A) LENCTH: 1200 base pairs
                 (B) TYPE: nucleic acid
                 (C) STRANDEDNESS: single
                (D) TOPOLOGY: linear
15
              (ii) MOLECULE TYPE: cDNA
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:137:
20
      CAGGCATGAG CAGAGCETTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGTAGE
       ACCTTCT986 GATTGGAATA CCCAACCAAG GGGGTATCCT TTACTCCTCA CTAGAGTACT
                                                                                          3.20
       TOGRARANGO COTGORGGAS CTUSCROCAG COTTTOCUGS TERTUSCTOS TERSETTOSS
                                                                                          130
       COGCOGACRA ATACGOOGIC AAAAACOGCA ACCACOTGAA TITTTTCCAG GAACTGGCAG
                                                                                          240
       ACCTOMATOS TOAGOTUATO AGOCTBATOO ACGACCAGGO CAACGGGGTO CAGACGACGO
                                                                                         300
       GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC
25
                                                                                         380
       TGACCTACAT CCCGGTCGTC GGGCACGCCC TATCGGCCGC CTTCCAGGCG CCGTTTTGCC
      TGACCTACAT CCCGGTCGTC GGGCACGCCC TATCGGCCGC CTTCCAGGCG CCGTTTTGCG
CGGGCGCGAT GGCCGTAGTG GGCGGCGCGC TTGCCTACTT GGTCGTGAAA ACGCTGATCA
ACGCGACTCA ACTCCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTGGGG GCCGCCATTG
CGGACATCAT TTCGGATGTG GCCGGACATCA TCAAGGGCAC CCTCGGAGAA GTGTGGGGAGT
TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA
CCGGACTGTT CTCTCGAGGG TGGTCGAACC TGGAGTCCTT CTTTGCGGGC GTCCCCGGCT
TGACCGGCGC GACCAGCGGC TTGTCGCAAG TGACTGGCTT GTTCGGTGC GCCGGTCTGT
CCGGACTGTC GGGCTTGGCT CACGCGGAT TGCCCGCC CTCGCCGCC
30
                                                                                          780
                                                                                         880
       TOGCCSGCAT TGGGGGGGGG TCCGGTTTTG GGGGCTTGCC GAGCCTGGCT CAGGTCCATG
                                                                                        900
35
      COSCOTORAC TOGGOROGOO CTRONGCOOC GROCTORTOS COCNOTOGGO GOOGGTOCOG
                                                                                        860
      ACCAGÉTOR COSECASTOS CACOTOSTOT ODEOSCAGOS TECCAASST ATSOSCOGAC 1020
      COGTAGUCAT GGGCGGCATG CACCOCTCTT CGGGGGCGTC GARAGGGACG ACGACGAAGA 1080
      ACTACTORIA ACCORDEGE GOGGECACTS AAGACGCOGA GCCCCCCCCA GTOGRAGCTG 1140
      ACSCGGGCSS TOUGCAAAAG GTGCTGGTAC GAAACGTCGT CTAACGGCAT GCCGAGCCAA 1200
40
      (2) INFORMATION FOR SEQ ID NO:138:
              (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 392 amino acids
45
                 (B) TYPE: amino scid
                 (C) STRANDEDNESS: single
                 (D) TOPOLOGY: linear
              (ii) MOLECULE TYPE: protein
50
              (xi) SEQUENCE DESCRIPTION: SEQ ID NO:138:
       Met Ser Arg Ala Phe Ile Ile Asp Pro Thr Ile Ser Ala Ile Asp Gly
                                                1.0
55
       Leu Tyr Asp Leu Leu Gly Ile Gly Ile Pro Asn Gln Gly Gly Ile Leu
                                           28
       Tyr Ser Ser Leu Glu Tyr Phe Glu Lys Als Leu Glu Glu Leu Als Als
```

	Ala	256 50	Buo	Gly	Asp	Gly	TYP	Leu	wiy	Ser	Ala	A18	Asp	59%	ZÄZ.	Ala
	Gly		Asn	Arg	Asn	His	~ ~	Asn	Phe	Phe	Gln	~ ~	7.697	Ala	gañ	Leu
	65					70					75				~	80
Ĭ	Asp	Arg	Gln	Leu	Ile 85	ser	Leu	rie	His	Asp 90	Gla	Als	Asn	Als	Val 98	Gln
	Thr	Tax	Arg	Asp 100	Ile	Løu	elu	Gly	Ala 105	Pär	Lys	Gly	Deu	Glu 110	Phe	Val
~ 4	Arg	Pro	Val	x_{1x}	Val	Asp	Leu	Thr	Tyr	lle	pro	Val	Val	Gly	Eis	Ala
10		_	115		w.X	w/0	N	730	rest si			an N	125		n 2:	v
		130					135	Pro				140				
a s	145					150		Leu.			155					160
15					165			Ala		170					175	
				180				Asp	185					190		
20			195					Tie 200					205			
		210					215	Gly				220				
شور يشر	228					230		Fhe			235					240
25					245			Gln		250					255	
				260				Leu	285					270		
30			275					Als 280					288			
		290					295	Gln		·		300				
as €.	305					310		Gly			338					320
35					325			val		330					335	
				340				Oly -	348					350		
40			355					77x					365			
		370					378	Val	GIU	ala	ರ್ಷ	380	ary	GTÀ	GTA	Gin
45	198 385	Vai	ueu	Val	YLÄ	390	val	AST								
	(2) 3	enpor	rmat)	CON 3	708 S	38Q]	D M):235) t							
50		{ ·	(A) (B) (C)	LENG	TH: 3: m UNDE	439 icle: XVES!	base ic a: i: s)	ingle	xs							
55		\$ 3	li))	OLE	COLE	TYPI	i ci	ma.								
		(2	ki) s	EQUI	ince	DES	rip	CION:	SE() ID	WO:3	39:				

ACCIPITACCO ATOCCOTOGO TECAGASCAA COCCAGACAA CACAAACTAG TCTAATTOOS 60

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TTATRAAJCA GACATTYCCO TOOTTATGTA GAAGATGTCS ACCGATCAGA TGAAGCGATC
      COCCTCACCT COTATCOCAT CTCTTTTCTC ACCATCCACC CCGTCGTCTT GCCAGCCCCCC
      ACCORGGACT TOUCGACGAT CONTACCOCC GTEAGTECTU GGAACACAGC CVTCTVTGCC
      COSACRACES SEGMENTACO COCTECTECO ARTEACOTOT COSTCOTESC GEOGGCOSE
 5
      TTCRCCGCGC ACACCAASCA CTACCGASTG GTGAGTAAGC CGGCGCGCT GGTCCATSGC
      ATCTTCCTCC CCCTCCCCCC GGCCACCGCC GATGCGTATG CGACCACCGA GGCCGTCAAT
                                                                                  420
                                                                                   439
      STSSTCSCSA CCSSTTAAS
     (2) IMPORMATION FOR SEC ID NO:140:
10
             (i) SEQUENCE CHARACTERISTICS:
               (A) LENGTH: 1441 base pairs
               (B) TYPE: mucleic soid
               (C) STRANDEDNESS: single
15
               (D) TOPOLOGY: linear
             (ii) MOLECULE TYPE: cDNA
             (xi) SEQUENCE DESCRIPTION: SEQ ID NO:140:
20
      GAGGTTGCTG GCAATGGATT TCGGGCTTTT ACCTCCGGAA GTGAATTCAA GCCGAATGTA
      TTCCGGTCCG GGGCCGCAST CGATGCTAGC CGCCGCGGCC GCCTGGGACG GTGTGGCCGC
                                                                                   120
      GGAGTTGACT TCCGCCGCGG TCTCGTATGG ATCGGTGGTG TCGACGCTGA TCGTTGAGCC 180
      OTOGATOGOG CCOSCOGCOG CCGCGATOGC GGCCGCGGCA ACGCCGTATG TGGGGTGGCT
                                                                                   240
      GGCCGCCACG GCGGCGCTGG CGAAGGAGAC GGCCACACAG GCGAGGGCAG CGGCGGAAGC
25
                                                                                   300
      GTTTGGGACG GCGTTCGCGA TGACGGTGCC ACCATCCCTC GTCGCGGCCA ACCGCAGCCG 360
      GTTGATGTCG CTGGTCGCGG CGAACATTCT GGGGCAAAAC AGTGCGGCGA TCGCGGCTAC
                                                                                  430
      CCAGGCCGAG TATGCCGAAA TGTGGGCCCA AGACGCTGCC GTGATGTACA GCTATGAGGG
                                                                                  4.90
      OSCATOTOCO OCCOSCOTOCO COTTOCCOCO OTTCACTCCA CCCGTGCAAG GCACCGGCCC
                                                                                  540
      GGCCBCSCCC GCGGCCCCAG CCGCGGCSAC CCAAGCCCCC CSTGCGGGCG CCGTTGCCGA
30
                                                                                  600
      TECRCAGGOG ACACTGGCCC AGCTGCCCCC GGGGATCCTG AGCGACATTC TSTCCGCATT
                                                                                   660
      GGCCGCCAAC GCTGATCCGC TGACATCGGG ACTGTT808G ATCGCGTCGA CCCTCAACCC
                                                                                  720
      OCAAGTCOGA TOTOCTCAGO CGATAGTGAT COTTACCCCG ATAGGGGAAT TEGACGTGAT
                                                                                  780
      COCCCTCTAC ATTRCATCCA TCGCGACCGG CAGCATTGCG CTCGCGATCA CGAACACGGC
                                                                                   840
                                                                                  900
35
      CAGACCUTEG CACATOSSOC TATACEGGAA OBCDESCOG CTGGGACCOA OSCASOSCCA
      TOTACTERST TOTACERCOS ACERSOCUER SCOSCACTES DECOCTTOS SEGRECOCOSC
      GCCGGTGTCC GCGGGCGTCG GCCACGCAGC ATTAGTCGGA GCGTTGTCGG TGCCGCACAG 1020
CTGGACCACG GCCGCCCCGG AGATCCAGCT CGCCGTTCAG GCAACACCCA CCTTCAGCTC 1080
CAGCGCGGC GCCGACCCGA CGGCCCTAAA CGGGATGCCG GCAGGCCTGC TCAGCGGGAT 1140
4()
      GECTTTEGCG AGCCTEGCCS CACGCGGCAC GACGGGCSGT GGCGGCACCC GTAGCGSCAC 1200
CAGCACTGAC GGCCAAGAGG ACGCCCCCAA ACCCCCGGTA GTTGTGATTA GAGAGCAGCC 1200
GCCGCCCGGA AACCCCCCCC GGTAAAAGTC CGGCAACCGT TGTGGCGCCG GCGGAAAATG 1320
CCTGGTGAGC GTGGCTATCC GACGGGCCGT TCACACCGCT TGTAGTAGCG TACGGCTATG 1390
      GAUGAUGGTG TUTGGATTUT OGGUGGUTAT CAGAGUGATT TTGUTUGUAA UUTUAGUAAA 1440
45
                                                                                  2442
     (2) INFORMATION FOR SEQ ID NO:141:
             (i) SEQUENCE CHARACTERISTICS:
50
               (A) LENGTH: 99 amino acids
               (B) TYPE: amino acid
               (C) STRANDEDNESS: single
               (D) TOPOLOGY: linear
55
             (11) NOLECULE TYPE: protein
             (xi) SEQUENCE DESCRIPTION: SNQ ID NO:141:
```

	Met 1	Ser	The	Val	Thx 5	Ile	Gln	Pro	Val	Val 10	Leu	Ala	Ala	Ala	Thr 15	Gly
	qaA	Leu	Pro	Thr 20	Tle	Gly	Thr	Ala	Val 25	Ser	Ala	ärg	Asn	30	Ala	Val
5	Cys	Ala	Pro 35	Thr	Thr	Gly	Val	Leu 40	Pro	Pro	Ala	Ala	Asn 45	āep	Val	Ser
		50			Ala		55					60				
10	55				Ala	70				-	75					80
				Ala	Asp 85	Ala	IAL	Aia	"inr	Thr 90	Giu	Aia	Val	Asn	88 887	AgT
	83.8	unr	uay													
15) (2) INFORMATION FOR SEQ ID NO:142:															
	(i) SEQUENCE CHARACTERISTICS:															
	(A) LENGTH: 423 amino acids															
20			(B) (C)	TYPI		onia	acia	ã								
			(\mathfrak{D})						v.							
		. (3	ii) r	(OLE)	CULE	TYPE	E: p:	rote:	in							
25		(ii) MOLECULE TYPE: protein														
	(xi) SEQUENCE DESCRIPTION: SEQ ID NO:142:															
	Met 1	Asp	Phe	gly	Leu S	Læu	Pro	Pro	Glu	Val 10	Asn	Ser	ger	Arg	Met 19	ljan
30	Ser	Gly	Pro	Gly 20	Pro	Glu	Ser	Net	lou 25	Ala	Ala	Ala	Als	Ala 30	Trp	Asp
	GJY	Val.	Ala 35	Ala	Glu	Læu	Thr	Ser 40	Ala	Ala	Val.	Ser	Tyr 45	Gly	Ser	Val
35	Val	ser so		Leu	Tle	Val	Glu 55		Trp	Net	Gly	Pro 60	Ala	Ala	Ala	Ala
			Ala	Ala	Ala			Tyr	val	Gly			Ala	Ala	Thr	
	SS Ala	Læu	ala	Lys	Glu	70 Thu	Ala	Thr	Glm		75 Arg	Ala	Ala	Ala	91u 95	86 Ala
40	Phe	gly	Thr	Ala 100	85 Phe	Ala	Net	Thr	Val 105	90 90	Pro	Ser	Leu	Val 110		Ala
	ass	Arg			Len	Met	Ser			Ala	Ala	Asn			Gly	Gln.
	Asn	Ser	115 Ala	Ala	Ils	Ala	Ala	120 Thr	Glm	Ala	Giu	Tyr	125 Ala	Glu	Net	Trp
45		730			Ala		232					140				
	145					150					155					160
	Ala	Ser	Ala	Lowis	200 165	Pro	Phe	Thx	Pro	Pro 170	Val	ain.	GIA	Thr	01y 175	Pro
50	Ala	Gly	Pro	Ala 180	ala	Ala	Ala	ala	%l& 185		Gln	Ala	Als	Gly 190	Ala	Gly
	Ala	Val	Ala 195	Asp	Ala	Gln	Ala	Thr 200		Ala	Gln	Leu	Pro 208	Pro	gly	lle
55	Leu	Ser 310		Ile	Len	Ser	Ala 215		ala	Ala	Asn	Ala 220		Pro	Leu	Thr
	Ser 225		Leu	Leta	gly	11* 230	Ala	Ser	Thr	Læu	Asn 235	Pro	Gln	Val	giy	Ser Zeo
		gln	Pro	lle	Val.		Pro	Thr	Pro	Ile		Glu	Leu	Asp	Val	

					245					250					285	
	Ala	Lsu	Tyr	11e 260		Ser	Ile	Ala	Thr 265		Ser	Tle	Als	Leu 270		Ile
ş	The	Asn	Thr 275	Ala	Ang	Pro	Trp	380 380	lle	GIA	Leu	Tyr	01y 285	Asn	Ala	Gly
	Gly	Leu 290	Gly	Pro	Thr	Gln	Gly 295		Pro	Leu	Ser	ser 300	Als	Thr	Asp	Glu
	305		Pro			310					318					320
10			Gly		325					330					335	
			Thr	340					345					350		
15			388 388				.,	360					365			
		370	Gly				375					380				
20	385		Thr			390					395					400
<i>\$29.0</i> *			Asp Gly		405			85.00	2.25.4	410	837	***	wed	2.4.0	415	\$6.200
	223	200	es es Ta	420	2732,627	25,35,450	.a.r.gg		,							
25	(2)	info	rmati	com i	808 I	SEQ :	m ci	0:14)	3 ;							
		\$:	i) Si													
					rii Bi ai				8.5688							
30			(C)	STRI	nedei Ologi	MES	3: S	ingl	2							
		€:	ii) i	OLE(CULE	TYP	S: pi	rote	is							
35		{ :	xi) s	EQUI	ENCE	DES	CRIP:	TION	: SE	ar c	NO:	L43:				
	Met 1	Ser	Leu	Leu	Asp 5	Ala	His	Il*	Pro	Gln 10	Leu	Val	Ala	Ser	Gla 15	Sor
4()	Ala	250	Ala	Ala 20	Lys	Äla	Gly	Leu	Met 35	Ärg	His	Thr	Ile	Gly 30	Gln	älä
	Glu	Gln	ala 35	Ala	Met	Ser	Ala	Gln 40	Ala	Nhe	His	Gla	Gly 45	Glu	Ser	Ser
d e		50	Phe				55		·			60				
45	\$5		Thr			70					78					80
		Thr	Tyr	LEV	Ala 85	Ala	ysb	Ala	Ala	Ala 90	Ala	Ser	Thr	Tyx	Thr SS	gly
50	Phe															
	(2)	info	RMAT:	con i	FOR E	ga:	ED NK	3:14	i t							
E &		(:	l) sı													
55					ath 8: 80				rds							
			$\{C\}$	STR	moss	WES:	B: \$1	ingle	3							
			$\{D\}$	TOP	hrogi	fo Li	(Mean)	e e								

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:144:

5 Cys Arg Leu Cys Leu Asp Ser His Leu Arg Val Val Ala Leu Pro Als 10 Gly Gln Pro Gly Arg Leu Val Gln Ala Ile Gly Pro Ala Gln Glu Arg 28 10 Asp Val Gly Gln Thr Arg Cys Thr Arg Thr Gly Leu Asp Xsa Val Ser 40 Ala Leu Thr Ala Ala Gin Fhe Ala Ala His Ala Gin Ile Tyr Gin Ala 55 60 Val Ser Ala Gin Ala Ala Ala Ile His Glu Met Phe Val Asn Thr Leu 15 70 75 Gin Xsa Xsa Ser Gly Ser Tyr Ala Ala Thr Glu Ala Ala Aso Ala Ala Ala Ala Cly

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